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Listing first 45 summaries
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1 atgacggaacaggccatctc.....agctcaagaaggtgatctaa 897
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Compositions and methods for determining interactions of

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AUTHORS	RESULT 1 AX134720 LOCUS DEPINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	00100000000000000000000000000000000000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No. Sco
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nger, W., Wile Davis, R.E.	897 b Patent WOO1328 4271237 man) oa; Chordata; ia; Primates;	10 BC004570 10 MMU27316 110 MMU27316 110 MMU27315 110 MMANTAP 110 MMANTAP 110 MARNAANC 5 AFC31347 5 BC043821 9 BC008664 10 AC122916 2 AC1350772 2 AC135265 2 AC135265 2 AC112888 2 AC111573 2 AC112888 6 AX301846 6 AX301846	6 AXI34720 6 AX301848 6 AX301848 9 EC0031912 9 EC007295 9 EC007735 9 EC007735 9 EC007775 9 EC008737 4 EC0268737 4 EC0268737 5 AX337175 6 AX40944 7 AC125887 7 AC125887 7 AC125887 8 AB009386 8 AB00938	SUMMARIES
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/mol_type="genomic DNA"
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RESULT 2 AX301848	AX301848 897 b
DEFINITION ACCESSION	AA3U1040 3 from Patent W00185944. AX301848 1 GT-17382965
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Me Mammalia; Eut
REFERENCE	son,C.M., Davis,R.E., Clevenger,W., Wiley,S.E., Mill
TLE	Y. and Carroll, A.K. ocator (ant), novel ant
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BASE COUNT	/organism= nome saprems /mol_type="genomic DNA" /db_xref="taxon:9606" 174 a 274 c 287 g 162 t
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Qy	1 ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC 60
Db	ATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGC
Qy	61 ATCTCCAAGACGGCCGTGGCTGCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC 120
Db	<pre>NAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCC</pre>
Qy :	8
Db :	121 GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC 180
Qy :	181 ATCCCCAAGGAGCAGGGCTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC 240
Db	181 ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCCAACCTTGCCCAACGTCATTCGC 240
Qy :	241 TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG 300
Db .:	241 TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG 300
Qy	301 GGGGGCCTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC 360
Db 	301 GGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC 360
Qy	361 GGTGCGGCCGGCGCGCTCCCTCTGCTTCGTGTACCCCGCTGGATTTTTGCCAGAACCCGC 420
Db	361 GGTGCGGCCGGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
Qy	421 CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC 480
Вb	421 CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC 480
Qy	GAT
В	GTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTC
Qy	541 GIGCAGGGCATCATCATCTACCGGGGGGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC 600
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through the I.M.A.G.E. Consortium/LIML at: http://in
Series: IRAK Plate: 42 Row: p Column: 5
This clone was selected for full length sequencing b
passed the following selection criteria: Similarity
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Submitted (06-JUN-2002) National Institutes of Hea
Gene Collection (MCC), Cancer Genomics Office, Nat
Institute, 31 Center Drive, Room 11A03, Bethesda,
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                Sequencing Center
Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL:
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               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="LocusID: 293"
/db_xref="taxon: 9606"
/clone="MGC: 29984 IMAGE: 5141625"
/tissue_type="Cervix, carcinoma"
/clone_lib="NIH_MGC_12"
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                                            CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG
                                                                                                                                                ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
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/db_xref="GI:21594693"
/translation="MYEQAISRADFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
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LVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQ
TYTAVAGVVSYPEDTYRRRMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWS
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/protein_id="AAH31912.1"
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le translocator), member 6"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Institute for Systems Biology
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ANUP Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Anup Madan, Rachel Dickhoff, Jessica Fahey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.series: IRAL Plate: 2 Row: n Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 9956
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1193)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                /organism="Homo saplens"
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/clone="McC:2387 IMAGE:2824067"
/tlssue_type="fung_small_cell_carcinoma"
/clone_lib="NHH_MGC_7"
/lab_host="DH10B-R"
/note="Yector: pOTB7"
94 . 990
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                                                                                                                       /translation="MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
IAADKQYKGIVDCIVRIPKEGGYLSFWRGNLANVIKYFPTQALNFAKDKYKQIFIGG
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LVKITKSDGIRGLYQGFSVSVQGIIIYRAAYEGVYDTAKGMLDDRKNTHIYVSWMIAQ
TVTAVAGYVSYPFDTYRRRMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWS
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                                                                                                      NVLRGMGGAFVLVLYDELKKVI'
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(mitochondrial carrier; adenine nucleotide
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/db_xref="GI:14286274"
  99.8%;
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Score 895.4;
Pred. No. 1.1
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    .4; DB 9;
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                                                                Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, mRNA (cDNA clone MGC:15671 IMAGE:3349670), complete cds.
                                               BC007295.1 GI:13938330
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AL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 22 Row: m Column: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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and Margolin,J.E.
Direct Submission
Submitted (24-JUL-2000) Human Genome Sequencing Center and Text
Submitted (24-JUL-2000) Human Genome Sequencing Center and Text
Children's Cancer Center, Baylor College of Medicine, Houston,
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1 (bases 1 to 1344)

Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A. A 'double adaptor' method for improved shotgun library construction anal. Blochem. 236 (1), 107-113 (1996)
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Yu.W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W., Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
Large-scale concatenation cDNA sequencing
Genome Res. 7 (4), 353-358 (1997)
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sapiens clone CDABP0051
                                                                                                                                                                                                                                                                                              /PICTEAL_LA="AAG01998.1"
/PICTEAL_LA="AAG01998.1"
/PICTEAL_LA="AAG01998.1"
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/LABSIALLQN="MIEDAISFAKDFLAGGIAAVIRY FPTQALNRAFTKKKYQIFLGG
TAADKQYKGIVDCIVRIPKEQGVLSFWRGNLANVIRY FPTQALNRAFTKKYGIFLGGC
UKITKSGGIAGATSLCFVY PLDFARTRLAADVGKSGTEREFRGIGGC
LVKITKSGGIAGATSLCGVY PLDFARTRLADVGKSGTEREFRGAGG
LVKITKSGGIAGATSLCGVY PLDFARTRLAGGLAGGTKTHIVYSKWIAQ
TVTAVAGVVSYFEDTVRRRMANGSGRKGADINYTGTVDCWRKIFRDEGGKAFFKGAWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1*
/codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="from patient with acute lymphoblastic leukemia" 90. .986
                                                                                                                                                                                                                                                                                       NVLRGMGGAFVLVLYDELKKVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
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/db_xref="taxon:9606"
/clone="cphap90051"
/clone_lib="constructed by Y.T.M. Tsang"
/dev_stage="infant"
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                                                                                                                                                                             99.88;
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                                                                                                                                                            0;
                                                                                                                                                          Score 895.4; DB 9;
Pred. No. 1.1e-131;
0; Mismatches 1;
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                                                                         REFERENCE
AUTHORS
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VERSION
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BC007850
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330 TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
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                                                                  Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1366)
Direct Submission
Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                         BC007850 1366 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, clone MGC:14294 IMAGE:4136545, mRNA, complete cds.
                                                                                                                                                                           Homo sapiens (human)
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through
Series:
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi.R.
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through the I.M.A.G.E. Consortium/LLNL at: http://image.lln
Series: IRAL Plate: 20 Row: 1 Column: 14
This clone was selected for full length sequencing because
passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                          GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC
                                                                           ATCCCCAAGGAGCAGGGCTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC
                                                                                                                             GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC
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cgapbs-r@mail.nih.gov
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/db_xref="G1:14043791"
/db_xref="G1:14043791"
/db_xref="G1:14043791"
/translation="MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
/translation="MTEQAISFAKDFLAGVIRYEPTQALMFAFKDKYKQIFLGG
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LVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVYDTAKGMLPDFKNTHIVVSWMIAQ
TVTAVAGVVSYFEDTVRRRMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWS
NVLRGMGGAFVLVLYDELKKYI"
a 419 c 409 g 251 t
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/clone_lib="NHH_MGC_19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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/product="Similar to solute carr
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/db xrof-"
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/clone="MGC:14294 IMAGE:4136545"
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BC014775.1 GI:15928607
                                                                                                                                                                                                        Direct Submission
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MCC), Cancer Genomics Office, National Cancer Gene Collection (MCC), Cancer Genomics Office, National Cancer Gene Collection (MCC), Cancer Genomics Office, National Cancer General National Cancer C
                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiu DNA Sequencing by: Baylor College of Medicine Hum
                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                  NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                              Strausberg, R.
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Mammalia; 1
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Sequencing by:
uencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
Muzny,D.M., Gibbs,R.A.
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Web site:
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                                                                                                             GGTGCGGCCGGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC
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/tissue_type="Cervix, carcinoma"
/clone_lib="NHH MGC_12"
/lab_bost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /POTEIN_Id="AAH14775.1"
//db_xref="G1:19928608"
/db_xref="G1:19928608"
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/translation="MTEDAISFARDFLAGGIAANVIRYEPTOALNFAFKDKYKQIFLGG
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TVTAVAGVVSYFPDTVRRRMMOPGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAMS
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(mitochondrial carrier; adenine nucleotide translocator),
member 5"
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93. .989
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                                                                                                                                                                                                                                     Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: National Institutes of Health Intramural
DNA Sequencing by: National Institutes of Health Intramural sequencing Center (NISC), Gaithersburg, Maryland;
Gaithersburg, Maryland;
Web site: http://www.nisc.nlh.gov/
Contact: nisc_mgc@nhgri.nlh.gov/
Contact: htsp://www.nisc.nlh.gov/
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Brooks,S., Benjanin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Benjanin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta-J., Ho,S-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Direct Submission

Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC008737 1466 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, clone MGC:3042 BC008737
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1466)
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REMARK COMMENT

Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAL Plate: 5 Row: o Column: 23 This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency http://image.llnl.gov information can be found

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                                             GTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
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  ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
                              GTGCAGGGCATCATCTACCGGGGGGGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
                                                                                     CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
                                                                                                    CTGGTGAAGATCACCAAGTCCGACGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
                                                                                                                                             CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:3042 IMAGE:3342722"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
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protein_id="AAH08737.1"
protein_id="AAH08737.1"
/db_xref="GI:14250567"
/db_xref="GI:14250567"
/translation="MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
IAADKQYKGIVDCIVRIPKEQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGG
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LVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQ
TYTAVAGGYVSTPFDTVRRRMMAQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWS
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/product="Similar to solute carrier family
(mitochondrial carrier; adenine nucleotide
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Two bovine genes for mitochondrial ADP/ATP
differences in various tissues
Biochemistry 28 (2), 866-873 (1989)
80720003
                                                                                             <u>,...</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
Eukaryota; Metazoa; Chordata;
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                                                                       ATGACGGAACAGGCCATCTCCTTCGCCAAGGATTTCCTGGCCGGGGGCATCGCCGCCGCC
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                                                                                                                                                                                                                                                                                      note="The span given
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91.5%;
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Cetartiodactyla; Ruminantia; Pecora;
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                                                                                              gene sets
                                                                                                       Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                     AX337175 1116 bp | F
Sequence 7684 from Patent WO0194629,
AX337175
                                                                 Avalon
                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                      AX337175.1 GI:18127894
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                 Pharmaceuticals
                                                                            WO 0194629-A 7684 13-DEC-2001;
                           Location/Qualifiers
1. .1116
/organism="Homo sapiens"
/mol_type="genomic DNA"
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                           AX409449 1116 bp 1
Sequence 2096 from Patent WO0229103
AX409449 AX409449.1 GT:21442154
Homo sapiens (human)
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Pred. No. 4.3e-112;
0; Mismatches 3;
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Patent: WO 0229103-A 2096 11-APR-2002;
GENE LOGIC INC (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                          GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGCATCCGGGGGCCTGTACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTT
                                                                      GACTGTTGGAGGAGATCTTCAGAGAGATGAGGGGCCAAGGCCTTCTTCAAGGGTGCGTGG
                                                                                                             CGGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTC
                                                                                                                                                                                     ATCGCGCAGACCGTGACGCCGTGGCCGTGGTGTCCTACCCCTTCGACACGGTGCGG
                                                                                                                                                                                                                                              GATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATG
                                                                                                                                                                                                                                                                                                     GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC
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                                                                                                                                                                      ATCGCGCAGACCGTGACGGCCGTGGCCGTGGTGTCCTACCCCTTCGACACGGTGCGG
                              TCCAACGTCCTGCGGGGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAG
                                                        GACTGTTGGAGGAAGATCTTCAGAGATGAGGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession
/note="EMBL GenBank Accession
330 c 346 g 209 t
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Original source text:
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1 (bases 1 to 1116)
1 (bases 1 to 1116)
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/db_xref="GI:339723"
/db_xref="GI:339723"
/db_xref="GI:339723"
/translation="LOVOHASKQIAADKQYKGIVDCIVRIPKEQGYLSFWRGNLANVI
RYFPTQALNFAFKDKYKQIFLGGYDRHAFWRYFAGNLASGGAAGATSLCFVYPLDFAR
RYFPTQALNFAFKDGYKQTFLGGYDRHAFWRYFAGYLOFSVSVQGIIIYRAAYFGYYD
TRLAADVGKSCTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGYYD
TAKGMLPDFKNTHIVVSMMIAQTVTAVAGVVSYPFDTVRRMMQSGRKGADIMYTGT
VDCWRKIFRDEGGKAFFKGAWSNVLRGMGAFYLVLYDELKKVI"
a 330 c 346 g 209 t
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/mol_type="mRNA"
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Allen, C., Allen, H., Alsbrooks, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cener, Y., Chen, Z., Chu, J., Cheveland, C., Cockeell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cockeell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Calderon, J., Cheve, J., Chen, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Duya, K., Durbin, K., Duval, B., Eaves, K., Brank, C., E., Falls, T., Fan, G., Fernandez, S., Finley, M., Flaggy, N., Forbes, L., Foster, M., Foster, P., Fraser, C., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerra, W., Hawis, S., Hadun, S.L., Hederson, N., Hernandez, J., Harvisk, P., Hawes, A., Henderson, N., Hernandez, J., Harvisk, P., Hawes, A., Henderson, N., Hernandez, J., Hallins, B., Howells, S., Hulyk, S., Hume, J., Idebird, D., Jackson, A., Karpathy, S., Kelly, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowar, C., Kraft, C., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Lorgado, R., J., Liu, X., Ma, J., Lu, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae;
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AC125887.3 GI:25008671
HTG; HTGS_PHASE1; HTGS_
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В õ 밁 Ş 밁 δõ 밁 Š В QY 밁 Ş 밁

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Direct Submission

AL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23269681.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas sembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence cantigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 291762) 3 (bases 1 to 291762) 3 (bases 1 to 291763) 3 (bases 1 to 291764) 3 (base
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TITLE JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

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REFERENCE AUTHORS TITLE

JOURNAL

----- Genome Center

Center: Baylor College of Medicine Center code: BCM

web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Conter project name: GWLD
Center project name: GWLD
Center clone name: CH230-274J3
Center clone name: CH230-274J3
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 23653 bases at least Q20
Consensus quality: 233437 bases at least Q20
Estimated insert size: 233445; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.igsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "vorking draft" sequence. It currently

* consists of 13 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

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BASE COUNT
ORIGIN
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                               where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:,
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                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mappi Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RPII-57/H4 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
AL354854
                                                                                                                                                                                                          SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced g1:14625557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                      http://www.chori.org/bacpac/home.htm
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                                           103872 CAGTCCCGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 103931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103572 CTGGCAGCCGACGTGGGAAAGTCAGGCACGGAGCGCGAGATTCCGAGGCCTGGGAGACTGC 103631
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                                                                 721 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780
                                                                                                                                                 421 CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTTCCGAGGCCTGGGAGACTGC 480
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  781 ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840
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/Clone=lib="RPCI-11.2"
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/138178. .138261
/note="Sequence from overlapping clone RPI1-27103
/note="Sequence from overlapping clone RPI1-27103
(AL353783). Assembly confirmed by restriction digest."
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/mol_type-"genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
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Db 103932 ATCTTCAGAGATGAGCGGGGCGAGGCCTTTTTCAAGGGTGTGGTCCAACGCCTCAAA 103991

Oy 841 GGCA-----TGGGGGGGCGCCTTCGTGCTGCTGCTACGACCTCAAG 885

103992 GGCATGGGGGTGGGGGCTTCGTGCTGGTCCTGTACGACGAGCTGAAG 104042

Search completed: August 24, 2003, 04:35:27 Job time: 3697 secs

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alifiers ANT3"		tri-F tion; tidiabe idiabe thera disease c neur tic ac ss; hy	translocator ANT3 cDNA.			BP.	ALIGNMENTS	ABX47259	AAX39617	ABN74435 ABT.61797	ABT09322	ABI.20966	ABX71399	AAS68190 AAD33664	ABS76969	AAS79610 ABS76857	ABN74319	ABK84798	AAS29836 AAS35083	ABL20967	ABS55029 ABS33737	ABZ83302	AAS05901 AAS16688	AAD00519	AAV36479	AAV36480	AAS05902	AAD00520	ABK63420	ABQ56282	ABN95598
		ANT3; mitochondria; ADP; ATP; hosphate; apoptosis; MPT; cancer; neuroprotective; nootropio; stic; anticonvulsant; neuroleptic; peutic; screening; psoriasis; e; Huntington's disease; dystonia; copathy; schizophrenia; MELAS; idosis; stroke; MIDD; perproliferative disorder; ss.							t cancer	Bovine embryonic g	Phase-1 Rat CT gen	Drosophila melanog	Human metabolism-a	DNA encoding novel	Frog embryonic gen	DNA encoding novel	Bovine embryonic g	Human cDNA differe	Human cytoskeletal DNA #33 encoding h	Drosophila melanog	Human TRICH encodi	Toxicologically re	adenine	in adenine n	cDNA.	Anti cDNA. Mus sp	Human adenine nucl	Human adenine nucl	equence	Human ovarian anti	96 u

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzhelmer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, capetris hereditary optic neuropathy, schizophrenia, mitochondrial diabetes and deafness (MIDD), and myoclonic disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic capilepsy red ragged fibre syndrome. The present sequence is a cDNA cenceding adenine nucleotide translocator ANT3 from human brain.
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Matches 897
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                                                CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGGTTCCGAGGCCTGGGAGACTGC
                                                                                                                GGTGCGGCCGGCCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
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                                                                                                                                                                                                                                                                                             TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGCAGATCTTCCTG
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                                                                                           GGTGCGGCCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC
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99US-0393441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 897; DB 21; Length 897; 100.0%; Pred. No. 1.3e-175; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clevenger W, Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e nucleotide translocator for potential therapeutic agents
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                                                                                                                                                                                                    Murphy AN, C. Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                             03-NOV-2000; 2000WO-US30535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenine nucleotide translocator-3 (ANT-3) cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS05903;
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                                                New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MTT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                       (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                     03-NOV-1999;
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                                                                                                                                      WPI; 2001-291054/30
P-PSDB; AAU01200.
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                                                                                                                                                                                                         Davis
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Best Local S
Matches 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes for human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability translition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
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                                                                                                                                     CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
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Pred. No. 1.3e-175;
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell an culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                               translocator nucleic acid
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P-PSDB;
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Zhao
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                                                             Sequence
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2000US-0552317.

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The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful coin gene therapy. A composition containing a polypeptide or polynucleotide coin gene therapy. A composition containing a polypeptide or polynucleotide coin gene therapy. A composition containing a polypeptide or polynucleotide coin gene the used to treat diseases of the peripheral nervous system diseases, such as a peripheral nervous injuries, peripheral neuropathy and coincalised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic coincalised neuropathies and central nervous system disease, amyotrophic cointeral solerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity chemotactic/chemokinetic activity, haemostatic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and cointers. The sequence data for this patent did not form part of the printed of specification.
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R, Drmanac RT;
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13-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                               28-JUL-2000; 2000US-222469P
08-JAN-2001; 2001US-260483P
                            (BAND/) BANDMAN O.
                                                                                                                                                              08-JAN-2002; 2002US-0044090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC are differentially expressed in activated vascular tissue. The invention relates to a combination comprising several cDNAs that CC are differentially expressed in activated vascular tissue. The invention CC also discloses a high throughput method for detecting differentially CC expressed cDNAs in a sample. The cDNAs of the invention may have antiatreriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic; CY gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a may be used in gene therapy. The cDNAs of the invention may be used in a compound that specifically binds a cDNA of the compound that specifically binds a cDNA of the compound that specifically binds a cDNA of the compound that specifically binds to the protein. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or crecombinant protein from a sample or purify a natural or crecombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of creatment of a vascular disease, e.g. atherosclerosis, cancer, coronary creativation injury, restenosis, or stroke. The cDNAs can also be used coronary constructed acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic coronary active diseases associated with abnormalities in the expression, coronary coronary active diseases associated with abnormalities in the expression, correpresents a cDNA of the invention that is differentially expressed in coronary active diseases associated with abnormalities in the expression.
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Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly frat http.seqdata.uspto.gov/sequence.html?DocID-20020137081.
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         GCGGTGCGGCGGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCC
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Pred. No. 1e-170;
0; Mismatches 1;
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Indels Length

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29-MAR-2001;
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16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in disease model; toxicological testing; transcript imaging;
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2001US-280067P.

2001US-280068P.

2001US-291280P.

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O, Yap PE, Amshey SR;
DA, Kleefeld Y, Gerstin
AJ, Panzer SR, Harris B;
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identifying encoded by h human diagnostic and therapeutic polypeptide useful for ifying test compound which specifically binds to a polyped by human diagnostic and therapeutic polynucleotide, a antibodies y binds to a polypeptide polynucleotide, and to

Claim SEQ ID No 573; 591pp; English.

The invention relates to novel human diagnostic and therapeutic complynucleotides designated dithp (ACC46080-ACC46749) and to their concoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp CDNA compositions comprising a dithp nucleic acid sequence; the creombinant production of DITHP proteins; antibodies specific for DITHP proteins; antibodies specific for DITHP compounds using a dithp hybridisation of Governments which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of compounds using a dithp hybridisation the compounds which specifically bind a DITHP protein; and methods of compounds using a dithp hybridisation compounds which specifically bind a DITHP protein; and methods of conditions including cancer and other cell probe. Dithp nucleic acid sequences and DITHP protein may be used in the conditions including cancer and other cell conditions including ftp.wipo.int/pub/published_pct_sequences.

Sequence 2213 BP; 422 A; 751 Ç 633 <u>.</u> 407 Η, 0 other;

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Length

2213;

Š 밁 Ş 밁 δã 밁 δÃ 밁 Q 밁 Query Match Best Local S Matches 817 386 181 121 266 206 al Similarity 817; Conserv 61 TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC Conservative 0; Score 816.4; DB 25 Pred. No. 5.6e-159; 0; Mismatches 1; 0; Gaps 240 385 180 325 120 265

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                        WPI;
                                                               Beazer-Barclay Y, Weissman
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity -

Claim 1; SEQ ID No 332; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (C (GCA), by detecting the level of expression of gene(s) (GS) identified by CC DNA chip analysis as given in the specification, and comparing CC GC, where differential expression level in an unactivated CC GC, where differential expression of GS is indicative of GCA. CC Also included are modulating (M2) GA by contacting GC with an agent CC that alters the expression of at least one gene in Gs; (2) screening (M3) GC for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a Subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from Gs, where CC the level of expression in a sample of the tissue of jene(s) from Gs, where CC inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue, M1 is useful for detecting a tissue having en cC inflammation with an agent that modulates the expression of gene(s) from GS in the tissue, M1 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening an agent capable of modulating GCA; M3 is useful for screening M3 is governed to ftp.wipo.int/pub/published_pct_sequences.

Sequence 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other;

Qy δÃ 밁 δõ 문 밁 멍 밁 Query Match Best Local S Matches 786 181 121 166 106 226 786; 61 Similarity GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTT CTGCAGGTCCAGCACGCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATTCGTG AACCTGGCCTCCGGCGGTGCGGCCGCCGCCGCTCCTCTCTTCGTGTACCCCGCTGGAT AACCTGGCCTCCGGCGGTGCGGCCGGCCGCGCTCCTCTGCTTCGTGTACCCCGCTGGAT AAGCAGATCTTCCTGGGGGGGGGTGGACAGACACGC---GTTCTGGAGGTACTTTGCGGGC AAGCAGATCTTCCTGGGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGC GACTGCATTGTCCGCCATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTT CTGCAGGTCCAGCACGCCAGCAAGCAGTACGAGCAGTACAAGGGCATCGTG Conservative 86.0%; 0; Score 771.2; DB 24; Length Pred. No. 1e-149; Mismatches ω, Indels <u>ω</u> 297 405 237 345 180 285 120 225 60 165

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TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA

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   The invention relates to progression of liver can
                                                                                         Diagnosing and detecting hepatocellular carcinoma involves detecting the leliver tissue sample -
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                                                     TCCAACGTCCTGCGGGGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGACCTCAAG
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tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, and toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
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Sequence 1116 BP; 231 A; 330 C; 346 G; GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTAC GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGCTCCTTCTGGAGGGGCCAACCTT GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTT Pred. No. 1e-0; Mismatches Mismatches 1e-149; 209 T; 0 other; 24; Ψ Indels Length 1116; ÿ Gaps 405 237 345 180 285 165 120 225 60

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778 AAGGTGATCTAA 789

ABL69347 standard; DNA; 1116

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XX III 15-M2
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05-JUN-2000;
18-SEP-2000;
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26-SEP-2000;

26-SEP-2000;

27-SEP-2000;

27-SEP-2000;

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27-SEP-2000;

28-SEP-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL69347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2000;
25-SEP-2000;
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                                                               (AVAL-) AVALON PHARM.
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2000US-209473P
2000US-231133P
2000US-234004P
2000US-234004P
2000US-234509P
2000US-234924P
2000US-234924P
2000US-235082P
2000US-235082P
2000US-235082P
2000US-23563PP
2000US-235637P
2000US-236034P
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Best Local
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Conservative

0;

86.0%;

Score 771.2; DB 24; Pred. No. 1e-149; Mismatches

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The present invention describes a method (M1) for screening for an carti-neoplastic agent. The method involves exposing cells to a chemical cargent to be tested for anti-neoplastic activity determining a change in carginal to be tested for anti-neoplastic activity determining a change in comprises a sequence (S) selected from 8447 sequences (given in ABL61664 cc comprises a sequence (S) selected from 8447 sequences (given in ABL61664 cc carginal to (S), where a change in carginal to (S), where a change in carginal to (S), where a change in carginal to an be used in gene therapy. All can be used for screening cc an anti-neoplastic agent, and can be used for producing a product which cresult of M1, and the data is sufficient to convey the chemical cc treatment of cancer such as colon, breast, stomach, lung, thyroid, cc oesophageal, ovarian, kidney, prostate or pancreatic cancer, infilitrating ductal cancer, cifil cancer, papillary carcinoma, clear cell cancer, infiltrating ductal cancer, cc carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 7684; 44pp; English.
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Sequence 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other;
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al Similarity 786; Conserv 286 AAGCAGATCTTCCTGGGGGGGCGTGGACAAGCACACGCAGTTCTGGAAGGTACTTTGCGGGC 345 226 GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTAC 418 526 238 181 166 GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTT 106 CTGCAGGTCCAGCACGCCAGCAAGCAGCAGCCGCCGACAAGCAGTACAAGGGCATCGTG 61 Н GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTAC GACTGCATTGTCCGCATCCCCAAGGAGCAGGGGCGTGCTGTCCTTCTGGAGGGGCCAACCTT CTGCAGGTCCAGCACGCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTG ATCGCGCAGACCGTGACGGCCGTGGCCGGCGTGTGTTCCTACCCCTTCGACACGGTGCGG GATACGGCCAAGGGCATGCTCCCCGACCCCCAAGAACACGCACATCGTGGTGAGCTGGATG GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAG 525 TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA 465 AAGCAGATCTTCCTGGGGGGGGGGTGGACAGACACGC---GTTCTGGAGGTACTTTGCGGGC ATCGCGCAGACCGTGACGGCCGTGGCCGGCGTGTCCTACCCCTTCGACACGGTGCGG GATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATG GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAG TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA AACCTGGCCTCCGGCGGTGCGGCGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGAT 297 237 180 120 225 60 645 477 417 357

Augustus

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Carter KC,

Ebner R,

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RESULT 11
ABQ56282
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrou PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; peurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                   Claim
                                                                                                                                                                                                                          Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2000; 2000US-209467P
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                                                                                                                                                                                                                   neurological
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DB; ABP43205.
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                                                                                                                                                                                  No 2162;
                                                                                                                                                                                                                                                                                                                                              CA;
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Matches 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), end disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and to shock syndrome), inflammatory conditions (e.g., mastitis, oophorit vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erytheme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification, at ftp.wipo.in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed ication, but was obtained in electronic format directly from WIPO .wipo.int/pub/published_pct_sequences.
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                                                                                                                  ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTG-AGCTGGATGATCGCCGAGACCGT
                                                                                        GTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
                                                                                                                                                                                           CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAAGGCCTGGGAGACTGC
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97.4%;
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GACGGCCGNGGCCGGCGNGG 687

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CC compounds or the progression of these toxic effects by determining the CC global changes in gene expression in tissues or cells exposed to the CC toxin and comparing these to gene expression in unexposed tissues or CC effect of a compound or progression of a toxic effect, preferably the CC hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or CC expression in a tissue or cell sample exposed to the compound of two or CC more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression. CC The method can also be used to identify an agent which modulates the CC toxic response and predict cellular pathways that a compound modulates specifically hybridises to a gene listed in the specification, a computer cC system comprising a database containing information identifying the cxpression level in a tissue or cell sample exposed to a hepatotoxin of a cell sted in the specification. The method is useful for elucidating global CC changes in gene expression level in a tissue or cell of at least one gene containing information used to present information cC changes in gene expression and for identifying the useful for elucidating global contained in the specification of a containing information and toxicity markers in drug screening and toxicity markers for the prediction or identification or identification of the physiological state of tissue or cell express and containing information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell
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15-MAY-2001;
22-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat sequence differentially expressed in response to a hepatotoxin #1327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining
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02-NOV-2000;
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2001US-292336P.
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2001US-297457P.
2001US-298884P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 other;
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916 GGCATGGGGGGTGCTTTTGTATTGGTATTGTATGATGAGAGATCAAAAAATATGTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
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                                   GGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA
                                                                                                                                                                        CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780
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                                                                    ATTGCAAAAGATGAAGGACGCAAAGCTTTCTTCAAAGGTGCTTGGTCCAACGTACTGAGA 915
                                                                                                            ATCTTCAGAGATGAGGGGGGGAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840
                                                                                                                                                                                                                           ACAGCCGTGGCGGGGCTGGTGTCCTATCCATTTGACACTGTCCGTCGTAGGATGATGATG 795
                                                                                                                                                                                                                                                                                                      ATGCTGCCAGACCCCAAGAATGTGCACATTATTGTGAGCTGGATGATTGCCCCAGAGTGTG
                                                                                                                                               CAGTCTGGCCGGAAAGGGGCTGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG 855
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Matches 709
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12-JAN-2001;
12-JAN-2001;
                                                                 The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                         Identifying an insulin receptor signaling modulator, useful as ditargets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling
                                                                                                                                                                                                                                                                                                                                      Seidel-Dugan
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                                                 Sequence
                                                                                                                                                                                                                          Disclosure; Page 159-160; 232pp;
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)B; AAO18516.
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Similarity 79.0%;
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Pred. No. 1.2e-113;
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                                                                                                                                                                                   ACGGCCGTGGCCGGCGTGTTCCTACCCCTTCGACACGGTGCGGCGGCGCGCATGATGATG
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AAD00520 standard; CDNA; 897 ₽₽

AAD00520;

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT2 cDNA.

Human; nucleotide translocator; ANT2; mitochondria; ADP; ATP;

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                                                                                                                                                                                                       The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability translation pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, cheber's hereditary optic neuropathy, schizophrenia, mitochondrial diabetes and deafness (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is a cDNA cenceding adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                Matches 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprofective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzhaimer's disease; Parkinson's disease; Huntington's disease; dystonia diabetes; teber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                                                                                                                                      Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 165-166; 175pp; English.
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                                                                                                                                                          66.3%;
78.9%;
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                                                                                                                                                          Score 594.6; DB 21
Pred. No. 2.4e-113;
                                                                                                                                              Mismatches 189; Indels
                                                                                                                                                                           DB 21; Length 897;
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SULT 15
S05902
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D AAS05902 standard; cDNA; 897 BP
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OT 07-SEP-2001 (first entry)

Human adenine nucleotide translocator-2 (ANT-2) cDNA sequence

Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss. Homo sapiens.

Key

Location/Qualifiers
CDS

/*tag- a

/product= "ANT-2"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes for human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transport of Angles across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. ANT) fused to an energy transfer molecule (ETM) protein compression construct can alter mitochondrial membrane permeability expression construct can alter mitochondrial membrane permeability components. The methods are useful for screening for agents that alter components. The methods are useful for screening for agents that alter dysfunctional cell survival. Such as Alzheimer's disease, diabetes components acell survival such as Alzheimer's disease, diabetes components acell survival such as Alzheimer's disease, diabetes components. The methods are useful for screenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy AN, C
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-2000; 2000WO-US30535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperproliferative disorders e.g. cancer, and deafness.
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                                                                    TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
GGTGGTGTGGACAAGAGAACCCAGTTTTGGCGCTACTTTGCAGGGAATCTGGCATCGGGT
                               GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCCAACCTGGCCTCCGGC
                                                                                                                                                            ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC
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                                                                                                                                          ATTCCCAAGGAGCAGGAAGTTCTGTCCTTCTGGCGGGGTAACCTGGCCAATGTCATCAGA
                                                                                                                                                                                                              GCCAGCAAGCAGATCACTGCAGATAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT
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	GGCATGGGGGGCCCTTCGTGCTGGTCCTGTACGAGGAGCTCAAGAAGGTGATCTAA 897	841	Qy
840	ATTGCTCGTGATGAAGGAAGCCTTTTTTCAAGGGTGCATGGTCCAATGTTCTCAGA 840	781	В
840	ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG	781	Qy
780	CAGTCAGGGCGCAAAGGAACTGACATCATGTACACAGGCACGCTTGACTGCTGGCGGAAG	721	₽
780		721	Qy
720	ACTGCTGTTGCCGGGTTGACTTCCTATCCATTTGACACCGTTCGCCGCCGCATGATGATG	661	DЬ
720		661	Ωy
660	ATGCTTCCGGATCCCAAGAACACTCACATCGTCATCAGCTGGATGATCGCACAGACTGTC	601	DЬ
660		. 601	Q
600	GTGCAGGGTATTATCATCTACCGAGCCGCCTACTTCGGTATCTATGACACTGCAAAGGGA	541	Дb
600		541	Qy
540	CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCT	481	Db
540		481	Qy
480	CTAGCAGCTGATGTGGGTAAAAGCTGGAGCTGAAAGGGAATTCCGAGGCCTCGGTGACTGC	421	망
480		421	Qy
420	GGTGCCGCAGGGGCCACATCCCTGTGTTTTGTGTACCCTCTTGATTTTGCCCGTACCCGT	361	뭥
420		361	Qy

Search completed: August 24, 2003, 02:53:16
Job time : 317 secs

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Title:
Perfect score:
Sequence:
                                                                   Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                  Score
  895.4
895.4
858.4
850.8
                                                                  %
Query
Match
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897
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gb_est2: *
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em_estpl:*
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em_gss_mam:
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em_gss_mus:
em_gss_pro:
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BC035469
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BC035469 Homo sapi
BX419742 BX419742
AL545701 AL545701
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13	13	14	12																																		13		9
Q9484	25C	D0485	12615	BQ049443	BM808760	AL555797	BM471365	BU849938	BM803703	BG759040	BQ941868	BM558078	BQ955091	AL558781	AL535607	BX415022	AL533037	AL527028	BX415427	BU528404	BI084258	AL568304	BX447073	BX404094	BQ677977	BM476356	BX375098	AL550157	AL542077	BV423613	BX3/5536	BM554606	AL514420	AL557414	AL539376	AL540267	\vdash	BQ932832	AL534908
847	25063	530	BI261510 602953570	•	808760 AGENC				BM803703 AGENCOURT	BG759040 602710667	BQ941868 AGENCOURT	BM558078 AGENCOURT	BQ955091 AGENCOURT	AL558781 AL558781	AL535607 AL535607	BX415022 BX415022	AL533037 AL533037	AL527028 AL527028	BX415427 BX415427	BU528404 AGENCOURT	BI084258 602869762	AL568304 AL568304	BX447073 BX447073	BX404094 BX404094	BQ677977 AGENCOURT	BM476356 AGENCOURT	BX375098 BX375098	AL550157 AL550157	AI.542077 AI.542077	BVAD2613 BVAD2613	BX375536 BX375536	M55460	4420 /	AL557414 AL557414	AL539376 AL539376	×		AGENCO	AL534908 AL534908

ALIGNMENTS

RESULT 1

	REMARK COMMENT		JOURNAL	AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	ACCESSION VERSION	DEFINITION	LOCUS	BC013256
Email: cgapbs r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC	USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	Submitted (27-AUG-2001) National Institutes of Health, Mammalian	Strausberg, R.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1355)	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (human)	HTC.	BC013256.1 GI:15301544	iens, clone IMAGE:3865895, mRNA.	BC013256 1355 bp mRNA linear HTC 27-AUG-2001	

FEATURES

source

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.linl.gov Series: IRAK Plate: 13 Row: e Column: 10
This clone was selected for full length sequenting because it passed the following selection criteria: matched mRNA g1: 3820534
This clone has the following problem: no 5' EST match.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalonébcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 99.9
96; Conservative
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                                                                                                                                                                                           GCCAGCAAGCAGATYGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC 180
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GTGCAGGGCATCATCATCTACCGGCGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGGCTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGACGGAACAGGCCATCTCCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGCGGCCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCCAACCTGGCCTCCGGC
                                                                                                                                                                                                                                                                                                CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAAGACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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COMMENT
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
ORGANISM
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BC035469
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                       Query Match
Best Local
     Matches
                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bCm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowia, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 871
     ; 968
                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 13 Row: f Column: 9 Sequencing because it passed the following selection criteria: matched mRNA 91: 4503556 This clone has the following problem: no 5' EST match.

1. 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg,R.

Direct Submission
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Submitted (31-JUL-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1355 bp
Homo sapiens, clone IMAGE:3867130,
BC035469
BC035469.1 GI:22028373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1355)
  Similarity 99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA 988
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/note="Wector: GCMV-SPORT6"
                          99.8%;
     0,
  Score 895.4; DB 11; Length 1355; Pred. No. 8.4e-183; O; Mismatches 1; Indels 0;
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HTC 31-JUL-2002

Query Match Best Local

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             Homo sapien
Eukaryota;
                                                    CS0DF020YC16
BX419742
BX419742.1 G
EST.
                                                                                                        BX419742
BX419742
                                         Homo
                                                                                                                                                                                                                                                                                          CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC
                                                                                                                                                                                    GGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGACGAGCTCAAGAAGGTGATCTAA 897
                                                                                                                                                                                                                                       ATCTTCAGAGATGAGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG
                                                                                                                                                                                                                                                                                                                                               GTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
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5-PRIME, mRNA sequence.
  Chordata;
Primates;
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Catarrhini;
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Vertebrata;
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             Euteleostomi;
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genosco
Library was constructed by Life Technologies, a linvitrogen. This sequence belongs to sequence climore information about this cluster, see
http://www.genoscope.cns.fr/
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation
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Li, W.B., Gruber, C.,
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/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

a 365 c 354 g 210 t 27 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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97.8%;
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Technologies, a division of
gs to sequence cluster 10389
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/.6e-175;
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•	Query Match Best Local Similarity 98. Matches 878; Conservative	/tiss//clos/	source /clo		nvitrogen. Tr more informati http://www.ge cgi-bin/clust	Genoscope - Co BP 191 91006 H Email: segref Library was co	JOURNAL Unpublished COMMENT On Feb 15, 2001 the Contact: Genoscope	Eukaryota; Mammalia; CE 1 (bases RS Li,W.B., (VERSION AL545701.2 GI:31267 KEYWORDS EST SOURCE Homo sapiens (human) ORGANISM Homo sapiens	z g	RESULT 4 AL545701	Qy 840 GGCATGGGGG 	Qy 780 GATCTTCAGAGA Db 932 GATCTTCAGAGA	Qy 720 GCAGTCCGGGCG	Qy 660 GACGGCGTGGC 	Oy 600 CATGCTCCCCGA Db 752 CATGCTCCCCGA	Qy 541 GTGCAGGGCATC
	94.8%; Score 850.8; DB 9; Length 1201; 98.8%; Pred. No. 3.3e-173; tive 0; Mismatches 8; Indels 3; Gaps 2;	/tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="15t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized." 362 c 372 g 218 t 1 others	// /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSDD1009YH03"	reng Lidang Email: Lidangerifector.com ord: http://fulllength.invitrogen.com/ InVitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODIOO9CDO2QP1. Location/Qualifiers	INVITIOGEN. This sequence belongs to sequence cluster 1000; for more information about this cluster, see http://www.genoscope.ons.fr/ cg1-bh/cluster.cg1?seq=CSODIO9CD02QPl&cluster=10389.r. Contact : cg1-bh/cluster.cg1?seq=CSODIO9CD02QPl&cluster=10389.r.	National de Sequencage redex - France scope.cns.fr, Web : www.genoscope.cns.fr scope.cns.life Technologies, a division of	COMM LIBRALES and HOLHWALLEACHOUN 2001 this sequence version replaced gi:12878183. noscope	Eukaryota; Metazoa; Chordata; Craniata; Percendata; Eucereoscomi; Mammalla; Euthería; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201) Liw.B., Gruber,C., Jessee,J. and Polayes,D.		AL545701 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO09YH03 5-PRIME, mRNA sequence. AL545701	:	GGGCATGGGGGGGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA 897	GATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCG 839	GCAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAA 779	GACGGCCGTGGCGGCGTGGTGTCCTACCCCTTCGACACGGTGCGGCGCGCGC	CATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGT 659	GTGCAGGGCATCAT-CATCTACCGGGGGGCCTACTTCGGCGTGTACGATACGGCCAAGGG 599
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Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r:
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgirseq=CSDDF007BE10QP1&cluster=10389.r. Conta
Peng Liang Email: fliang@lifetech.com URL:
http://filllength.invitrogen.ccm/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF007BE10QP1.
Location/Qualifiers
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On Feb 13, 2001 this sequence version replaced
Contact:-Genoscope
Genoscope - Centre National de Sequencage
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                                                            CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
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/mol_type="mrNA"
/db_xref="taxon:9606"
/clone="CSODF007Y120"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
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/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDN
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
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949 bp
AGENCOURT_8824122 NIH_MGC_18 Homo
5', mRNA sequence.
BQ932832
BQ932832.1 GI:22348215
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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National Institutes of Health, M
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Mammalia; Eutheria; Primates;
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/note="Organ: lung; Vector: pOTH7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

a 305 c 297 g 173 t 2 others
                                                                                                                                                                                                                            /clone="IMAGE:6459460"
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Best Local :
922 b
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BQ226117 GI:20407526
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TITLE
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Matches 866;
     481 CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCCC
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Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.lnl.gov
plate: LLAM13324 row: 1 column: 19
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1 (base to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                     CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGGGGAGTTCCGAGGCCTGGGAGACTGC
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ilarity 96.7%;
Conservative
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Location/Qualifiers
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/mb_xref="taxon:9606"
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
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D; Mismatches 29;
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                                                                                                                                                                                                                         Email: sequencescope.cns.fr Web: www.genoscope.cns.fr was not normalized. Library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq~CSODF032CG01QP1&cluster=10389.r. Contact: Peng Liang Email: fliang@lifetech.com URL: http://tullength.invitrogen.com/InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODF032CG01QP1.
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On Feb 15, 2
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CS0DF032YN01
AL540267
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1 (bases 1 to 1201)
L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/Clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st s
was primed with a NotI-oligo(dT) primer. Five p
enriched, double-strand cDNA was digested with
cloned into the Not I and EcoRV sites of the pC
vector. Library was not normalized."
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/clone="CS0DF032YN01"
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/mol_type="mRNA"
                                                                                                                   /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
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No. 4.6e-170;
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31-MAY-2003

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1 (bases 1 to 1201)

1.1,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12868534.

Contact: Genoscope
Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODF033AH10Qp1&cluster=10389.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faradday Avenue Genoscope sequence ID: CSODF033AH10Qp1.
Location/Qualifiers
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                                CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
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/mol_type="mRNA"
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/clone="Organ: brain; Vector: pcmvSpORT_6; 1st strand cDNA was primed with a Not!-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMvSpORT 6 vector. Library was not normalized."
vector. Library was not normalized."
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On Feb 15, 2001 this sequence version repl
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1201)
L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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AL557414 Homo sapiens T CELLS (JURKAT CELL
Clone CSODH003YD19 5-PRIME, mRNA sequence.
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WCGACGAGCTCAAGAAGGTGATCTAA 1053	GGGCATGGGGGCCCCTTCGTGCTKGTCCTGTWCGACGAGCTCAAGAAGGTGATCTAA	995	
ACGACGAGCTCAAGAAGGTGATCTAA 897		839	
TCAAGGGTGCGTGCTCCAACGTCCTGC 994	GATCTTCAGAGAGGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGC	935	
TCAAGGGTGCGTGCTCCAACGTCCTGC 838		780	
ACGGGCACGTCCGACTGTTGGGAGGAA 934	CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACGTCCGACTGTTGGGAGGA	875	
ACGGGCACCGTCGACTGTT-GGAGGAA 779		721	
GACACGGTGCGGCGGC-SATGATGATG 874	ACGGCCGTGG-CGGCGTGGTGTCCTACCCCTTCGACACGGTGCGGCGGC-SATGATGATG	817	
GACACGGTGCGGCGCGCATGATGATG 720		661	
GTGAGCTGGATGATCGCGCAGACCGTG 816	ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG	757	
GTGAGCTGGATGATCGCGCAGACCGTG 660		601	
TTCGGCGTGTACGATACGGCCAAGGGC 756	GTGCAGGGCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC	697	
TTCGGCGTGTACGATACGGCCAAGGGC 600	- ດ	541	
GCCTGTACCAGGGCTTCAGTGTCTCC 696	CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC	637	
GGCCTGTACCAGGGCTTCAGTGTCTCC 540		481	

p mRNA linear ES (JURKAT CELL LINE) Homo EST 31-MAY-2003 sapiens cDNA

Euteleostomi;

2001 this sequence version replaced gi:12900994

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr was not normalized. Library was constructed by Life Technologies, a division of invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODH003CB10QPl&cluster=10389.r. Contact : Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitrogen Corporation 1600 Faradday Avenue Genoscope sequence ID: CSODH003CB10QPl.

/Organism="Homo sapiens"
//mol_type="mrNA"
//mol_type="mrNA"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
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//tissue_type="T CELLS (JURKAT CELL LINE)"
//cell_line="JURKAT CELL LINE"
//clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
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AL514420 Homo sapiens
CL0BB010ZF01 5-PRIME,
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                                                                                      ACGGCCGTGGCCGCGT-GGTGTCCTACCCCTTCGACACGCTGCGCGCGCGCGCATG-ATGA
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pp 191 91006 EVRY cedex - France
pp 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cg1/seq-CLOBBO10ZF01RP1&cluster=10389.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://tulllength.invitrogen.com/InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBBO10ZF01RP1.
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Full-length cDNA libraries
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Mammalia; Eutheria; Primates;
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CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGGAGTTCCGAGGCCTGGGAGACTGC
                                     GGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC
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nilarity 97.0%;
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/clone_lib="Homo sapiens NEUROBLASTOMA"
/clone_Tib="Homo sapiens NEUROBLASTOMA"
/note="Yector: pcMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned i the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."

346 c 370 g 219 t 33 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: MA.G.E. Consortium Library Preparation: MA.G.E. Consortium Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov Plate: LLAM12746 row: b column: 05 High quality sequence stop: 646. Location/Qualifiers 11071 /ocanism="Homo sapiens" /mol_type="mrNA" /db_xref="taxon:9606" /clone="IMAGE:5736868" /clone="THHONG (phage-resistant)" /note="Organ: small intestine; Vector: pcWV-SpORT6; Site_1: Not; Site_2: Sali; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NHLMGC Library."	BM554606 LOCUS BM554606 LOCUS DEFINITION AGENCOURT_6545407 NIH_MGC_88 Homo saplens cDNA clone IMAGE:5736868 ACCESSION BM554606 VERSION BM554606.1 GI:18794346 EVERYORDDS EST. SOURCE ORGANISM Homo saplens Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) COMMENT Email: cgapbs: femail.nih.gov Tisause Procurement: ATCC Tisause Procurement: ATCC Tisause Procurement: ATCC	### A CTGCCGGGCGTGGGAAAGTYAGGCACAGGCGCGCGTGTACCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCCAGGCCAGACCCGGCAGCCCAGGCCCAGGCCCAGGCCAGCCCAGGCCCAGGCCAGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGCCCAGGCCCAGCCCAGCCCCAGGCCAGCCCAGGCCCAGCCCAGGCCCAGCCCAGGCCAGCCCAGGCCAGCCCAGGCCAGCCCAGGCCAGCCCAGGCCAGCCCAGGCCAGCCCAGCCCAGGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGGCAGCCAGCCCAGGCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCACCCCCC
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Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODC014BD12QP1&cluster=10389.r.
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSODC014BD12QP1.
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1 (bases 1 to 1014)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone="CSODCO14YG24"
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
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Tissue Procurement: DCTD/DTP/Gazdar
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence
                    /clone="IMAGE:6424804"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIILMGC_18"
/clone_lib="NIILMGC
Superscript II
                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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             BX423613
BX423613.1 GI:30768310
                                         BX423613 1201 bp mRNA linear EST 1
BX423613 Homo sapiens FETAL BRAIN HOMO sapiens CDNA clone
CSODP034YB14 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                               CAGTCCCGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGGTGGAGGAAG
                                                                                                                                                                                                                                CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780
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499 GGTGCGGCCGGCGCACCTCCCTCTGCTTCGTTTCGTGTACCCGCTGGATTTTCGCCAGAACCCGC
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191 ATCCCCAAGGACAGGGCTGCTGTCCTTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC
319 ATCCCCAAGGACGAGGCGTGCTGCTCTTCTGGAGGGGCAACCTTGCCAACGTCATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                             199 ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                    61 ATCTCCAAGACGGCCGTGGCTCCGATCGATCCAAGCTGCTGCTGCTGCAGGTCCAGCAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

1 (Lyw.B., Gruber.C., Jessee,J. and Polayes,D. Pull-length cDNa libraries and normalization Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@enoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/
cg1-bin/cluster-g17seg-c5lAF009ZD08QP1&cluster=10389.r.
Peng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com/ InVitroGen Corporation
http://fulllength.invitrogen.com/ InVitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSIAF009ZD08QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                                                                                    TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
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ilarity 97.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="nRNA"
/mol_type="nRNA"
/mol_type="nRNA"
/db_xref="taxon:9606"
/clone="CSODF034YB14"
/tissue_type="FEFTAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
vector. Library was not normalized."
vector. Library was not normalized."
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Pred. No. 4.1e-164;
3; Mismatches 17;
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Indels Length 1201;

5

60

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378

420

498 360 438

ц	GCATGYGGGGGCGCCTCCGTGCTGGTCCTGTTCGACGAGCTCAAGAAGGTGATCTAA 1031	975	В
	GGCATGO	841	ν
974	ANC-TCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCACGTCCTGCGGG 974	916	용
840	CGTCCTGCGG	781	Ŋ
915	CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGCA-CGTCGACTGTTGGAGGGAG	857	8
780	CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG	721	Ą
856	ACGGCCGTGG-CGGCGTGT-CTACCCCTTCGACACGGTGCGGCGCGCATGAWGATG	799	용
720		661	υ
798	ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG	739	₽
660	- ଜ	601	Ŋ
738	GTGCAGGGCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC	679	岁
600	GTGCAGGGCATCATCATCTACCGGGGGGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC	541	Ų
678	CTGGTGAAGATCACCAAGTCCGGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC	619	용
540	CTGGTGAAGATCACCAAGTCCGAGGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC	481	ş

Search completed: August 24, 2003, 03:33:47 Job time: 2423 secs

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APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
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APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Weng, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Yunqing
APPLICANT: Wang, Zhiwei
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APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Domanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
FILOR APPLICATION NUMBER: US/09/620,31
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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US-09-620-312D-687
                                                                                                                                                                                                                                                                                                Sequence 687, Applica Patent No. 6569662 GENERAL INFORMATION:
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PRIOR I
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (131)..(1027)
JS-09-620-312D-687
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US-09-257-991A-13498
US-09-257-991A-52580
US-09-257-991A-52580
US-09-257-991A-52580
US-09-257-991A-52580
US-09-257-991A-52580
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US-09-434-354-3
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Best Local S
Matches 897
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ALIGNMENTS	US-09-252-991A-10508 US-09-252-991A-10550 US-09-252-991A-10309 US-09-598-747-24 US-09-659-312D-63 US-09-702-705-1014 US-09-702-705-1014 US-09-704-914-3 US-09-144-914-3 US-08-125-468-1	US-09-252-991A-1128 US-08-617-801A-5 US-08-622-991A-952 US-09-622-991A-10583	US-09-252-991A-4103 US-09-252-991A-4055 US-09-252-991A-4141 US-08-252-991A-907
	Sequence 10508, A Sequence 10550, A Sequence 10309, A Sequence 24, Appl Sequence 63, Appl Sequence 1014, Ap Sequence 1014, Ap Sequence 3, Appli Sequence 1, Appli	Sequence 1128, Appli Sequence 5, Appli Sequence 95, Appli Sequence 95, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, 1583, A	

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Sequence 3, Application US/09434354

Patent No. 5562563

GENERAL INFERMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Murphy, Anne N.
APPLICANT: Miley, Sandra Elleen
APPLICANT: Miley, Alexander Y.
APPLICANT: Miley, Alexander Y.
APPLICANT: Davis, Robert E.
FITTLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FITTLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FITTLE OF INVENTION: INTERACTIONS AND METHODS FOR DETERMINING
FITTLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FITTLE OF INVENTION: INTERACTIONS AND METHODS FOR DETERMINING
FITTLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FITTLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FITTLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 660088.433

CURRENT APPLICATION NUMBER: US/09/434,354

CURRENT APPLICATION NUMBER: US/09/434,354

CURRENT APPLICATION NUMBER: US/09/434,354

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO
IENGTH: 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-434-354-3
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                                                                                                                                                                                                                                     TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
                                                                                                                  ATCCCCAAGGACCAGGGCGTGCTGTCTGGGAGGGCAACCTTGCCAAGGTCATTCGC
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; TYPE: DNA
; ORGANISM: Homo sapien
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
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Best Local S
Matches 708
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CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF EEQ ID NOS: 54
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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08; Conservative
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                                               GTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
                                                                                                              CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTTCAGTGTCTCC
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ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
                                                                                            CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCT
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                              GTGCAGGGTATTATCATCTACCGAGCCGCCTACTTCGGTATCTATGACACTGCAAAGGGA
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Pred. No. 7.6e-123;
0; Mismatches 189;
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; FEATURE:
; NAME/KEY:
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US-08-961-871-11
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 Query Match
Best Local Sin
Matches 706;
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Patent No. 6013858 ISSUED 01:11:00
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 109-8080
                                                                                                                                                                                             TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wallace, Douglas C.
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 5370 M
CITY: Boulder
STATE: Colorad
COUNTRY: US
                                                                                                                                                              STRANDEDNESS: double TOPOLOGY: not relevant
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                 Similarity
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     Conservative
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                                                                                                                                                 DNA (genomic)
               65.9%;
Score 591.4; Pred. No. 4.2e
0; Mismatches
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 .4; DB 3;
4.2e-122;
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US-08-961-871-9
                                                                                                                     Sequence 9, Application US/08961871 Patent No. 6013858 GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                   GGCATGGGGGGCGCCTTCGTGCTGCTGTACGACGAGCTCAAGAAGGTGATCTAA 897
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FILING DATE: 31-0CT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Dona M.
REGISTRATION NUMBER: 33.878
REFERENCE/DOCKET NUMBER: 78-96
TELEPONE: (303) 499-8080
TELEPAN: (303) 499-8080
TELEPAN: (303) 499-8089
INFORMATION FOR SEQ ID NO: 9:
SEQUIENCE CHARACTERISTICS:
LENGTH: 117 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 704; Conservative
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Best Local
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TOPOLOGY: not relevant
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: MUS musculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Green
STREET: 5370 Manl
CITY: Boulder
STATE: Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                  GGGGCAGCTGGGGCCACCTCCCTCTGCTTCGTCTACCCGCTGGACTTTGCTAGGACCACG
                                                                                                GGAGGCGTTGATCGACATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCCTCTGGT 453
                                                                                                                     GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC 360
                                                                                                                                                                            TACTTCCCCACTCAAGCCCTGAACTTCGCCTTCAAAGACAAGTACAAGCAGATCTTCCTG
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78.5%;
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Pred. No. 2.1e-121; 
0; Mismatches 193; Indels 0;
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US-09-434-354-1
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US-09-434-354-1
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
                                                                                                                                                                            Query Match
Best Local S
Matches 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application Patent No. 6562563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID N
SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                 Q ID NO 1
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il Similarity 77.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/09434354
                                                                                                                                                                          Score 564.2; DB 4;
Pred. No. 4e-116;
0; Mismatches 198;
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                                                                                                                                                                                                                                                                    Patent No. 6500938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Sequence 622,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for 1
                                                                                                                                                                                               APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                            STREET: 3174 PORTING CITY: PALO ALTO STATE: CALIFORNII COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                            GGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA 897
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                                                                                                              CALIFORNIA
                                                                                                                                             3174 PORTER DRIVE
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Sequence 38, Application US/08518878B Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
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Best Local Similarity 99.5%;
Matches 197; Conservative
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IMMEDIATE SOURCE:
LIBRARY: LIVETUT04
CTONE: 2517151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 622:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
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APPLICATION NUMBER:
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APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tartagila, Louis A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                          STREET: 1155 AVER
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ATCCCCAAGGAGCAGGGC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCA-TGTCCGC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC 212
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                                                                                                                                                                                                                                                                                                                                                              3: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/016,434
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Pred. No. 1.2e-32;
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TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/08294522B Patent No. 5741666 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COTUZZÍ, LAUTA A.
REGISTON NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 788
TELECOMMUNICATION INFORMATION:
     STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                     Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  869-9741/8864
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RESULT 8 US-08-518-878B-38

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                                                                                                                                                                           Sequence 38, Application US/08470868A
Patent NO. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.3%;
Best Local Similarity 45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 78: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 23-AUG-1994
                                    ZIP: 10036
                                                      COUNTRY:
                                                                                                              STREET:
                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                         561 TGACCTCATCAAGG 574
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Pred. No. 0.00074;
0; Mismatches 236;
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RESULT 11
US-08-807-861A-38
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                                                                                                                                           Sequence 38, Application US/08807861A Patent No. 5853975
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                                                                                                           GENERAL INFORMATION: APPLICANT: Tartag
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
                                           TITLE OF INVENTION: ME
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
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                              ADDRESSEE:
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          1155 Avenue of the Americas
                                                     Tartaglia, Louis A.
VENTION: METHODS AND COMPOSITIONS FOR THE
VENTION: REGULATION OF BODY WEIGHT DISORDERS,
EQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 790-90
(212) 869-8864
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version
                            Pennie & Edmonds LLP
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Pred. No. 0.00074;
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US-08-807-861A-38
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TELEPAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.3%; Score 56.4; DB 2; Length 1596; Best Local Similarity 45.6%; Pred. No. 0.00078; Matches 198; Conservative 0; Mismatches 236; Indels 0
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FILING DAYS.

CLASSIFICATION: 514

PRIOR APPLICATION UNDER: US 08/518,878

APPLICATION WINDER: US 08/470,868
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
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903 TGACCTCATCAAGG 916
                                          876 CGAGCTCAAGAAGG 889
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10036-2711
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                                                                                                                                GGATGTGGTAAAGGTCCGATTCCAAGCTCAGGCCCGGGCTGGAGGTGGTCGGAGATACCA 782
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US-09-210-681-38
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GENERAL INFORMATION:
APPLICANT: Tartag
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.3%;
Best Local Similarity 45.6%;
Matches 198; Conservative
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CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION UNUBER: 08/807,861

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

FILING DATE: 23-AUG-1994

FILING DATE: 23-AUG-1994
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/210,681
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696 CACGGTGCGGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACATCATGTACAC 755
                                                                          663 GAGCCGCCTCCTAGCAGGCACCACAGGTGCCCTGGCTGTGGCTGTGGCCCAGCCCAC 722
                                                                                                                            636 GAGCTGGATGATCGCGCAGACCGTGACGGCCGTGGCCGTGGTGGTGTCCTACCCCTTCGA 695
                                                                                                                                                                                                                                                                                                              516 CCTGTACCAGGGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTT 575
                                                                                                                                                                                                                                                                                                                                                                                  483 CCAGTACCGCGGTGTGATGGGCACCATTCTGACCATGGTGCGTACTGAGGGCCCCCGAAG 542
                                                                                                                                                                                                                           576 CGGCGTGTACGATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGT 635
                                                                                                                                                                                                                                                                                543 CCTCTACAATGGGCTGGTTGCCGGCCTGCAGCGCCAAATGAGCTTTGCCTCTGTCCGCAT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                 456 CGAGTTCCGAGGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGGCATCCGGGG 515
                                                                                                                                                                           CGGCCTGTATGATTCTGTCAAACAGTTCTACACCAAGGGCTCTGAGCATGCCAGCATTGG 662
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US-08-946-719A-38
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                                                                                                                                                   ; MOLECULE TYPE: US-08-946-719A-38
                                                         Query Match
Best Local Similarity 45.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/807,861
PRILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/470,868 FILING DATE: 06-JUN-1995 APPLICATION NUMBER: US 08/294,522 FILING DATE: 23-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08 FILING DATE: 26-FEB-1997 APPLICATION NUMBER: US 08 FILING DATE: 23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 8-CLASSIFICATION:
                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                           NAME:
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 483 CCAGTACCGCGGTGTGATGGGCACCATTCTGACCATGGTGCGTACTGAGGGCCCCCGAAG
                                    456 CGAGTTCCGAGGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGGCATCCGGGG 515
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E: New York
TRY: U.S.A.
10036-2711
                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08946719A
                                                                                                                                                                                                                                       1596 base pairs
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1155 Avenue of the Americas
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                                                                                       45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.30
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                                                                        0
                                                                      Score 56.4; DB 3;
Pred. No. 0.00078;
0; Mismatches 236;
                                                                                                         Length 1596;
                                                                        Indels
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                                                                      Gaps
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US-09-547-983-38
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INFORMATION
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,983
FILING DATE: 12-Apr-2000
CLASSIFICATION: -CURROWND
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDI
                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tartaglia,
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                                                                                                                                                          APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGCTCAAGAAGG 889
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                                  TELEFAX:
                                                                                                       NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                    (212) 869-9741/8864
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55 Avenue of the Amer
PENNIE
NO: 38
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                                                                                       7853-066
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INCLUDING OBESITY

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SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
HENCH: 1596 base pairs
STRANDENNESS: single
STRANDENNESS: single
HOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO
US-09-547-983-38
                                                                                               TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-07-16
EARLIER FILING DATE: 1997-07-16
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FBASEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1192
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US-09-142-565-1
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                                          ; TYPE: DNA
; ORGANISM: HOMO SAPIEN
US-09-142-565-1
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09142565A Patent No. 6187560
GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
APPLICANT: Kelly Paine
APPLICANT: RObert James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.3%;
Best Local Similarity 45.6%;
Matches 198; Conservative
Query Match
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     6.0%;
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     Score 54.2;
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     DB 3;
     Length 1192;
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788 TGGTGACCTACGACATCCTCAAGGAGA 814
                                    866 TCCTGTACGACGAGCTCAAGAAGGTGA 892
                                                                                                                                                          746 TCATGTACACGGGCACCGTCGACTGTTGGAGGAAGATCTTCAGAGATGAGGGGGGGCAAGG 805
                                                                                                                                                                                                                                        608 CAGATGTGGTGAAGGTCCGATTTCAGGCCAGCATACACCTCGGGCCATCCAGGAGCGACA 667
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                                                                           GCCTGTGGAAAGGAACTTTGCCCAACATCATGAGGAATGCTATCGTCAACTGTGCTGAGG
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Search completed: August 24, 2003, 05:34:13 Job time : 77 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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    US-09-811-094-3
897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1517243 seqs, 1124081882 residues
                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_NA: *
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/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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64.2	64.2	64.2	81.8	94.6	94.6	94.6	96.2	71.2	71.2	71.2	873.4	95.4	897	897	897	Score
62.9	62.9	62.9	64.9	66.3	66.3	66.3	66.5	86.0	86.0	86.0	97.4	99.8	100.0	100.0	100.0	Query Match Length DB
894	894	894	1711	897	897	897	1196	1116	1116	1116	2592	1212	897	897	897	ength
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US-09-185-904A-1	US-09-810-644-1	US-09-811-094-1	US-10-198-846-13437	US-09-185-904A-2	US-09-810-644-2	US-09-811-094-2	US-09-917-800A-1327	US-10-171-581-48	US-09-880-107-2096	US-09-969-708-213	US-10-044-090-152	US-10-037-270-687	US-09-185-904A-3	US-09-810-644-3	US-09-811-094-3	ID
_	Sequence 1, Appli	Sequence 1, Appli	Sequence 13437, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1327, Ap	Sequence 48, Appl	2096,	Sequence 213, App	Sequence 152, App	587,	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Description

53.8 2706 14 47.8 468 11 45.9 493 11 43.9 720 9 43.7 410 11 37.2 420 11 37.5 434 10 35.5 434 10 35.5 439 11 35.3 409 9 34.1 424 11 33.3 301 11 33.3 416 11 33.3 416 11 33.1 487 9 31.2 483 11 31.2 483 11 31.2 483 11 31.1 484 11 31.2 485 11 31.1 484 11 39.7 464 9 29.7 464 9 29.5 484 11 29.5 484 11		c 43	42	41	40	c 39	38	37	36	35	34	33	32	c 31	30	29	28	27	26	25	24	23	22	21	20	19	18	c 17
.8 2706 14 .9 448 11 .9 448 11 .9 720 9 0 .7 410 11 .5 420 11 .5 434 10 .5 434 11 .5 434 11 .3 409 9 0 .1 424 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .3 390 11 .5 483 11 .5 483 11 .5 484 11 .5 485 11 .5 486 10 .7 324 10 .7 474 19 .7 474 19 .8 1536 9 0	240.4	242.6	264.2	264.6	265.8	266.4	266.4	274	275	278.8	280	282.2	286.4	296	298.4	299	302.8	306	317	318.4	318.6	334	363.2	392.4	394	412	429	482.4
	26.8	27.0	29.5	29.5	29.6	29.7	29.7	30.5	30.7	31.1	31.2	31.5	31.9	33.0	33.3	33.3	33.8	34.1	35.3	35.5	35.5	37.2	40.5	43.7	43.9	45.9	47.8	53.8
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US-10-103-313-611 US-09-918-995-26014 US-09-919-995-9153 US-09-910-995-16539 US-09-918-995-3706 US-09-918-995-3706 US-09-918-995-3706 US-09-918-995-37003 US-09-918-995-37003 US-09-918-995-37003 US-09-918-995-37381 US-09-918-995-37388 US-09-918-995-37388 US-09-918-995-37388 US-09-918-995-37388 US-09-918-995-37388			11	11				11	10	10	14	11			H					Ξ	10	11	11	11		H	11	14
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ALIGNMENTS

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; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-811-094-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Scho, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
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                                                                                                                                                 Query Match
Best Local Similarity
Matches 897; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09811094 Patent No. US20010044144A1
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOOS, Walter H.

APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
  61
                  61 ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCTGCAGGTCCAGCAC 120
                                                                         ATCTCCAAGACGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC 120
                                                                                                                                                     100.0%;
ilarity 100.0%;
Conservative 0,
                                                                                                                                                       0;
                                                                                                                                                     Score 897; DB 9;
Pred. No. 5.3e-227;
Mismatches 0;
                                                                                                                                                                                            Length 897;
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Sequence 3, Application US/09810644

Patent No. US20020012992A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088:420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CUURENT APPLICATION NUMBER: US/09/810,644
CUURENT APPLICATION NUMBER: US/09/810,644
  RESULT 2
US-09-810-644-3
US-09-810-644-3
Sequence 3, App
GENERAL INFORM
APPLICANT: An
APPLICANT: An
APPLICANT: W
APPLICANT
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Matches 897
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SEQ ID NO 3
LENGTH: 897
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ORGANISM: Homo
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                                                                                                                                         ATCTTCAGAGATGAGGGGGGAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840
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Sequence 3, Application US/09185904A

Patent No. US20020177185A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: Description of ADENINE NU
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVE
TITLE OF INVENTION TRANSLOCATOR
TITLE OF INVENTION THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
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LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
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                                                        GTGCAGGGCATCATCTACCGGGGGGGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
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100.0%; Pred. No. 5.3e-227;
tive 0; Mismatches 0;
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RESULT 4
US-10-037-270-687
Cequence 687, Ap
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PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 687
LENGTH: 1212
                                                                                                                                                                                         ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(1027)
US-10-037-270-687
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TITLE OF INVENTION: NO. US20030104529Alel Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
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                                                                                    Chen, Rui-hong
Chen, Qing A.
Yehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
Tillinghast, John
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                                   ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGTCAAGCTGCTGCTGCAGGTCCAGCAC
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GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC
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Chen, Rui-hong
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Zhang, Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu, Chenghua
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                                                                                                                                         Conservative
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0; Mismatches
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WS-10-044-090-152
US-10-044-090-152
US-10-044-090-152
Sequence 152, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVERVION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
CITERET APPLICATION UNMERS US/10/044,090
CURRENT FILING DATE: 2002-01-09
RUMBER OF SEQ ID NOS:-850
SEQ ID NO 152
SEQ ID NO 152
SEQ ID NO 152
FEATURE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unisc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11
NAME/KEY: unisure
LOCATION: 1131, 1929
OTHER INFORMATION: a, t, c, g, or other
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        RESULT 6
US-09-969-708-213
; Sequence 213, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
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Pred. No. 9.9e-221;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 658
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 213
LENGTH: 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/0 CURRENT FILING DATE: 2001-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1116
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                      GATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATG
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              TCCAACGTCCTGCGGGGGGGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAG
                                                                                      CGGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTC
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Pred. No. 7.9e
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APPLICANT: Gene Logic, Inc.
FILE COF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
VINDBER OF SEQ ID NOS: 3350
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2096
LENGTH: 1116
TYPER: DNA
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APPLICANT: Vockle
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OTHER INFORMATION: Genbank Accession
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                                                                                                              GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGCATCCGGGGCCTGTACCAG
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                                                 GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC
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Scherf, Uwe
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APPLICANT: Linsley, Peter
APPLICANT: Mao Mao
TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
FILE REFERENCE: 9301-157-999
CURRENT APPLICATION NUMBER: US/10/171,581
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR FILING DATE: 2001-06-18
INUMBER OF SEQ ID NOS: 366
SEQ ID NO 48
LENGTH: 1116
TYPE: DNA
ORGANISM: HOMO SEPIENS
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2001-06-18
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Sequence 48, Application US/10171581
Sequencion No. US20030104426A1
BUBLICATION TONE
GENERAL INFORMATION
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Best Local 9
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    TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA
                                                                                      AACCTGGCCTCCGGCGGTGCGGCGCGCGCGCTCCCTCTGCTTCGTGTACCCGCTGGAT
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APPLICANT: Montael
APPLICANT: Johnson, Kory
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-50389.
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/22,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/22,880
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/290,336
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
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US-09-917-800A-1327
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                                            SOFTWARE: PatentIn
SEQ ID NO 1327
LENGTH: 1196
                                                                                                        PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-07-09 NUMBER OF SEQ ID NOS: 1740
ORGANISM: Rattus norvegicus
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538 ATCGCGCAGACCGTGACGGCCGTGGCCGGCGTGTGTCCTACCCCTTTCGACACGGTGCGG
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; Sequence 2, Application US/09811094

; Patent No. US20010044144A1
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Pred. No. 1.1e-147;
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APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willey, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: MOOS, Walter H.
APPLICANT: MOOS, Walter H.
APPLICANT: Pei, Vazhong
ITILE OF INVENTION: NOVEL ANT LIGANDS AN
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 897
TYPE: DNA
ORGANISM: Homo saplen
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ACGGCCGTGGCCGGCGTGGTGCCTACCCCTTCGACACGGTGCGGCGGGGGCGCATGATGATG
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nilarity 78.9%;
Conservative
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0; Mismatches
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APPLICANT: Anderson, Christen M.
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Scott W.
APPLICANT: Wiler, Scott W.
APPLICANT: Moos, Jounattra S.
APPLICANT: Moos, Sounitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILLE REFERENCE: 660088, 420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SEC ID NO 2
SEQ ID NO 3
SEC ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
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Patent No. US20020012992A1
GENERAL INFORMATION:
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Similarity 78.9%;
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GGTGCCGCAGGGGCCACATCCCTGTGTTTTGTGTACCCTCTTGATTTTGCCCCGTACCCGT 420
                                 GGTGCGGCCGGCCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
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APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley. Sandra Bileen
APPLICANT: Wiley. Sandra Bileen
APPLICANT: Wiley. Sountra S.
APPLICANT: Wiley. Scott W.
APPLICANT: Ghosh, Sounitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
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TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCR
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Similarity 78.9%;
08; Conservative
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Query Match Best Local :

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RESULT 13

US-10-198-846-13437

US-10-198-846-13437

Sequence 13437, Application US/10198846

Publication No. US20030099974A1

GENERAL INFORMATION:
APPLICANT: Lilile, James
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
ITILE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRITLE OF INVENTION: HERAPY OF BREAST CANCER

TITLE OF INVENTION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

UMMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13437
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 1397, 1398, 1399, 1400, 14
; LOCATION: 1416, 1417, 1418, 1419, 1420, 14
; LOCATION: 1426, 1427, 1428, 1429, 1430, 14
; LOCATION: 1426, 1427, 1428, 1429, 1430, 14
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1445, 1446, 1447, 1448, 1449, 17
; LOCATION: 1445, 1446, 1447, 1448, 1449, 17
; OTHER INFORMATION: n = A,T,C or G
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                  CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG
                                                                                         ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
                                                                                                                            ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC
                                                      CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
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 ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG
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Sequence 1, Application US/09811094

Patent No. US20010044144A1

GENERAL INFORMATION:

APPLICANT: LAVIS, Robert E.

APPLICANT: Davis, Robert E.

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiley, Sounitra S.

APPLICANT: Wiley, Sounitra S.

APPLICANT: Hoosh, Sounitra S.

APPLICANT: NOUEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

CURRENT APPLICATION NUMBER: US/09/811,094

CURRENT APPLICATION NUMBER: US/09/811,094

CURRENT FILENG DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 894

TYPE: DNA
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US-09-811-094-1
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al Similarity 77.6%;
696; Conservative
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                         CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 540
                                                                  TIGGCIGCIGATGIGGCAGG---CGCGCCCAGCGIGAGIICCATGGICIGGGCGACIGI 477
                                                                                                           CTGGCAGCGGACGTGGGAAAAGTCAGGCACAGAGCGCGAGGTTCCGAGGCCTGGGAGACTGC 480
                                                                                                                                                       GGGGCCGCTGGGGCCACCTCCCTTTGCTTTGTCTACCCGCTGGACTTTGCTAGGACCAGG 420
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-644-1
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: MOOS, Walter H.
APPLICANT: MOOS, Walter H.
APPLICANT: MOOS, Walter H.
APPLICANT: Pell Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEO IT NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                             Matches 696;
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          181 ATCCCTAAGGAGCAGGGCTTCCTCCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT 240
                                                181 ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC 240
                                                                                               121 GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC 180
                                                                                                                                                                                 61 ATCTCCAAGACGGCCGTGGCTGCGATCGAGCGGGTCAAGCTGCTGCTGCTGCAGGTCCAGCAC 120
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Similarity 77.6%;
36; Conservative
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pred. No. 2.9e-139;
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					de translocator; ANT3; mitochondria; adenosine tri-phosphate; apoptosis; adenosine tri-phosphate; apoptosis; ity transition; neuroprotective; noo tatic; antidiabetic; anticonvulsant; rotective; therapeutic; screening; prkinson's disease; Huntington's disease; Huntington's disease; tary optic neuropathy; schizophrenipathy; lactic acidosis; stroke; MIDD and deafness; hyperproliferative disragged fibre syndrome.	Human adenine nucleotide translocator ANT3.			298 AA.	ALIGNMENTS	ABR41715 AAW61169 ABU53219 AAW71031 AAW71031 AAW71031 ABU53219 ABU53218 ABU53218 ABB67300 ABB68380 ABB673205 ABB74106 AB74106 AB7
					Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzhelmer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.						Human DITHP organe Antl protein. Mus Human metabolisma Human metabolisma Human adenine nucl Novel human diagno Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Human metabolisma Human TRICH-19 pro Human ovarian antl Human TRICH-19 pro Human ovarian diagno Candida albicans e Novel human diagno Candida albicans e Novel human diagno Novel human diagno ADP/ATP carrier prarabidopsis thalia Arabidopsis thalia

Result

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SUMMARIES

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AAY71033 AAM39641 AAU01200 AAU10380 AAM41427 AAO18516 AAY71032 AAU01199 AAU011379

Human adenine nucl Human polypeptide Human adenine nucl Human adenine nucl Human insulin rece Human insulin rece Human adenine nucl Human adenine nucl

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RESULT 2
AAM39641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
  amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                          Human polypeptide SEQ ID NO 2786.
                                                                                                                                                    22-OCT-2001 (first entry)
                                                                                                                                                                                                                                        AAM39641 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 46; Page 173-174; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant construct encoding adenine nuclectide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson-CM, Davis RE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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Best Local :
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAI88642-AAI42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 2786; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful for treating such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
N-PSDB; AAI58797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š, Ž
                                                             181
                                                                                                                                                                                                                                                                                                                                                              298;
                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang Z,
Zhou P,
                   VGGIIIYRAAYEGYYDTAKGMLDDKNHHIVVSMMIAQTVTAVAGVYSYBDTVRRRMM
VGGIIIYRAAYEGVYDTAKGMLDDKNHHIVVSMMIAQTVTAVAGVVSYBFDTVRRRMM
VGGIIIYRAAYEGVYDTAKGMLDDKNTHIVVSMMIAQTVTAVAGVVSYBFDTVRRRMM
                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                           GAAGATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                           IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                   IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA;
                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0488725.

2000US-0553317.

2000US-0598042.

2000US-0520312.

2000US-0653450.

2000US-0653450.

2000US-06539305.

2000US-0693036.
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                                                                                                                                                                                                                                                                                                                                                       ; Score 1543; DB 22;
; Pred. No. 4.6e-157;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Length 298;
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Zhang J;
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                                                                                                                                                                                                                                                                    (ANT-3) protein. ANT proteins are mitochondrial permeability

C transition (MTP) pore components responsible for mediating transport

C of ADP across the mitochondrial inner membrane. ANT proteins interact

c with other mitochondrial core components e.g. cyclophilins to

c regulate MFT. The present invention relates to a novel nucleic acid

c expression construct comprising a promoter operably linked to a

c polynucleotide encoding a mitochondrial pore component polypeptide

c (e.g. ANT) fused to an energy transfer molecule (ETM) protein

c (e.g. ANT) fused to an energy transfer molecule (ETM) protein

c (e.g. ANT) fused to an energy transfer molecule (ETM) protein

c (e.g. The methods are useful for a fitochondrial membrane permeability

transition and/or alter the interaction between mitochondrial core

components. The methods are useful for screening for agents that alter

c MPT and/or cell survival. These agents are useful for the prevention or

c dysfunctional cell survival, such as Alzheimer's disease, diabetes

mellitus, Parkinson's disease, Huntington's disease, schizophrenia,

mitochondrial encephalopathy, lactic acidosis, stroke,

c mellitaratare a career and desfore
                                                                                                                                            Query Match
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynuclectide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial permeability transition mitochondrial core component; mitochon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU01200;
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                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 186pp; English.
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Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2001.
                                                                                                                                                                                                                                                     hyperproliferative
                                                                                    hes 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to energy transfer molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenine nucleotide translocator-3; ANT-3;
                                                                                                                  Similarity
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G, Davis RE;
                                                                                                                                                                                                       298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease;
                                                                                    Conservative
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                                                                                                                                                                                                                                                     disorders e.g. cancer, and
                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes
                                                                                                               0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiley SE,
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                                                                                    0
                                                                                                               Score 1543;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mellitus; hyperproliferative disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                    Mismatches
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                                                                               DB 22;
1.6e-157;
s 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑY,
                                                                                                                                                                                                                                                        deafness.
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                                                                                                                                      Length
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RESULT 4
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide ANT cuseful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, is useful for identifying an agent that binds to an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating the presence of an ANT polypeptide. ANT covalently bound to a solid phase. Detectably labeled ANT ligand is acvalently or non-cuseful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; adenine nucleotide translocator; ANT;
mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-055598/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MITO-) MITOKOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNYLRGMGGAFYLVLYDELKKYI 298
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Y, Carroll AK;
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0652450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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                                                                             N-PSDB; AAI60583.
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Wang Z,
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llarity 100.0%;
Conservative (
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Wehrman T, X
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                                                                                                                                                                  Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
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Pred. No. 4.6e-157;
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, Yang Y,
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

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RESULT 6
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   12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; insulin receptor signaling; insulin receptor signaling modifier; ISM; diabetes; metabolic syndrome; antidiabetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human insulin receptor signaling modifier SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2002 (first entry)
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                                                                                                                                                                                                     11-JAN-2002;
                                                                                                                                                                                                                                                                      18-JUL-2002.
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Side: The sequence data for this patent did not form part of the printed
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; 2001US-261226P.
; 2001US-261303P.
; 2001US-261304P.
; 2001US-261335P.
; 2001US-261336P.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 160-161; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contacting an assay system comprising insulin receptor signaling modifiers with a test agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seidel-Dugan C,
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                                                                                       QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                                                                                              VQGIIIYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                       GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                        GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLYKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                               IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                      MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                               VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
                                                                        QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
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2001US-261456P

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2001US-261532P

2001US-261539P

2001US-261539P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an insulin receptor signaling modulator, useful as treating diabetes or metabolic disorders, comprises
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2001US-261695P.
2001US-261697P.
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                                                                                                                                                                                                                                                                                                                                                              Score 1463; D
Pred. No. 1.8e
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              DB 23;
L.8e-148;
hes 8;
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AAY71032 standard; Protein;

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61

IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG

120 60

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(ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of constructs. ANT is a nuclear encoded protein and a major component of cinner mitochondrial membrane. It mediates transport of adenosine constructs are across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability corresponds to protests. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to cregulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated continuity of diseases, cancer, psoriasis, diabetes, dystonia, cleber's hereditary optic neuropathy, schizophrenia, mitochondrial cencephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative consequence, is an interesting diseases and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an according nucleotide translocator ANT2 from human brain.
                                                                                                                                                                 Query Match
Best Local
                                                                                                                                      Matches
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08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents
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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discloses a method to produce adenine nucleotide translocator
                                                                                                                                                                                                                                                                  298
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                                                                                                                                      13;
                                                                                                                                   Score 1454; D
Pred. No. 1.7e
l3; Mismatches
                                                                                                                               DB 21;
1.7e-147;
hes 9;
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The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact vith other mitochondrial core components e.g. cyclophilins to regulate MFT. The present invention relates to a novel nucleic acid components of the present invention relates to a novel nucleic acid components expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MFT and/or cell survival. These agents are useful for the prevention or dysfunctional cell survival. Such as Albeimer's disease, diabetes compliants, Parkinson's disease, Huntington's disease, schizophrenia, complete the provential encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondrial mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 186pp; English.
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Velicelebi G, Davis RE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andreyev AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frigeri LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclophilin;
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RESULT 9
AAU10379
ID AAU1
XX
AU10379
AC AAU1
AC AAU1
DT 14-F
XX
Huma
XX
Huma
XX
Huma
XX
Homo
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                           Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson CM, Davis
Ghosh SS, Moos WH,
                                                                                                                                                                                                                          Claim 44; Fig 2; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-055598/07.
N-PSDB; AAS16689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2001; 2001WO-US15416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200185944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human adenine nucleotide translocator 2 (ANT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU10379 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial matrix protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VQGIIIYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRHMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREERGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IPKEOGVLSFWRGNLANVIRYFPTOALNEAFKDKYKOIFLGGVDKHTOFWRYEAGNLASG 120
61 IPKEOGVLSFWRGNLANVIRYFPTOALNEAFKDKYKOIFLGGVDKRTOFWRYEAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenine nucleotide translocator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RE, Clevenger W, W
Pei Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.28;
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Pred. No. 1.7e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ws,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Szabo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nuclaic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell culturing the host cell. (I) is also useful for targeting a polypeptide

a polypeptide

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RESULT 10
ABR41715
ID ABR41715
AC ABR41
XX ABR417
XX DE Humar
XX Humar
XX Humar
XX Cance
KW Cance
KW Cance
KW Cance
KW Organ
XX OOS
DN WO20
DN
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Best Loc
Matches
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29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                   Human; dith; diagnostic and therapeutic polynucleotide; diagno cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metrabolic neurological disorder; gastrointestinal disorder; transport disornective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; disease model; toxicological testing; transcript imaging;
                                                                                                                                                                                                                                                                                                                                                                                     organelle-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR41715
                                                                                                                                                                                                        27-MAR-2002;
                                                                                                                                                                                                                                                  05-DEC-2002
                                                                                                                                                                                                                                                                                              WO200297031-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQVKGIVDCIVR
||:|:|||||||||:||:||:||:||
MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQVKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
2001US-279619P.
2001US-280067P.
2001US-2910607P.
2001US-29180P.
2001US-291829P.
2001US-291849P.
2001US-299428P.
2001US-299776P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organelle-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                      2002WO-US10056
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                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
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Pred. No. 1.7e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 23;
1.7e-147;
hes 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                            animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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Dufour GE, Hillman
Daughtery SC, Dam
Peralta CH, David
                                                                                                                                                               HYW.
                                                                                                                                                                                              (INCY-) INCYTE GENOMICS
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                                                                                                                                                              2003-129518/12.
                                                                                                                                                                        CH,
                                                                                                                                                                                  Jones AL,
, Hillman
                                                                                                                                                                      R MH C
                                                                                                                                                                                     Tran
                                                                                                                                                                             Yu JY,
Liu TF,
                                                                                                                                                                      LO A,
                                                                                                                                                                          Lewis
                                                                                                                                                                                      AB,
                                                                                                                                                                          SA,
                                                                                                                                                                      Lan RY,
                                                                                                                                                                         Dahl CR,
I Tuason
Nguyen
SA, Chen
                                                                                                                                                                         , Gietzen D, Chi
n O, Yap PE, Ams
n DA, Kleefeld Y,
n AJ, Panzer SR,
                                                                                                                                                                      Urashka ME;
                                                                                                                                                                                     Chinn
                                                                                                                                                                                  Amshey
                                                                                                                                                                              Gerstin
                                                                                                                                                                          8
                                                                                                                                                                             EH;
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Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polyencoded by human diagnostic and therapeutic polynucleotide, induce antibodies useful for ៥

N-PSDB; ACC46652

Claim 27; SEQ 日 No 1250; 591pp; English.

CC proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of for compounds which specifically bind a DITHP protein; and methods of CC assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the CC diagnosis of a wide variety of conditions including cancer and other cell CC proliferative disorders; autoimmune or inflammatory disorders; bacterial, CC viral, fungal or parasitic infections; hormonal disorders; metabolic CC disorders; neurological disorders; gastrointestinal disorders; transport CC disorders; neurological disorders; gastrointestinal disorders; transport CC screen for modulators of protein activity or gene expression. DITHP CC proteins can additionally be used in analysis of the proteome of a tissue CC rell type and to induce antibodies. The dithp nucleic acids are CC additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of continued antimal models of human disease or knock in human disease or knock in the present sequence represents a DITHP protein which is an organelle-cassociated protein. associated protein.

Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences. The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP not form part of the directly fro from WIPO

Sequence 429 A

Query Match Best Local

Similarity

91.9%; 95.2%;

2e-143;

DB

Length

429;

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                                                                                                                                                                                                                               Matches
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                                                        146
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                                                                     GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                      MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
             VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                             IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                      MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                               IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                            Score 1418; D
Pred. No. 2e-1
3; Mismatches
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RESULT 11
AAW61169
ID AAW61
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                                                                                                                                           Query Match
Best Local
                                                                                                                              Matches
                                                                                                                                                                                                                                 The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Tag dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports Any which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or gene therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antl; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 39-40; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graham BC, Macgregor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEM-) UNIV EMORY.
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                                                                                                                                                                                                                         independent of ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-286608/25.
DB; AAV36479.
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 61
                          61
                                                               H
                                                                                                                                             Similarity
                                                                          MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
                   IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                         OSGRKGADIMYTGTYDCWRKIFRDEGGKAFFKGA-W----SWYLRRMGGA 285
                                                                                                                                                                                           298 AA;
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                            91.5%; Score 1412; DB 19;
88.6%; Pred. No. 5.4e-143;
ive 19; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wallace
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A
                                                                                                                            Indels
                                                                                                                                                        Length 298;
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                                                                                                                          Gaps
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Query Match Best Local S Matches 263

Similarity

91.1%; 90.1%; 17;

Score 1406; DB 22; Pred. No. 2.3e-142; 7; Mismatches 12;

Indels Length 293;

0

Gaps

Conservative

G

61 65

1 ALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE

AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE 64

QGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG

124 60

120

QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAG

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RESULT 12
ABU53219
XX ABU53
XX ABU53
XX Human
XX Human
XX Homo
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                                                                    This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example III; Page 850; 1095pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHU-) GERMAN HUMAN GENOME PROJECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-2000; 2000WO-IB01496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human metabolism-associated DKFZphtes3_35n12 homologue #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAAGATSLCFVYPLDFARTTLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0149499.
99US-0156503.
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RESULT 13
AAY71031
ID AAY71031
XX AAY71
XX AAY71
XX AAY71
XX AAY71
XX AAY71
XX Human
XX Human
XX Human
XX Human
XX Alaha
KW Alaha
KW Alaha
KW Mitoo
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                    The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, leber's hereditary optic neuropathy, schizophrenia, mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dyst diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant construct encoding adenine polypeptide, useful e.g. in screening f against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; adenine nucleotide translocator; ANT1; mitochondria; adenosine di-phosphate; adenosine tri-phosphate; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myoclonic epilepsy red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiParkinsonian; cytostatic; antidiabetic; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondrial permeability transition; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
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DB; AAD00519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenine nucleotide translocator
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990S-0393441
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        lactic
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                                                                                                                                                                                                                                                                                                                                                                                                                        175pp; English
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     acidosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ
     stroke
schizophrenia, mitochondrial
stroke (MELAS), hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleotide translocator for potential therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ws,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Szabo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dystonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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Best Local
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                                                                                                  WPI; 200
                                                                                                                                Murphy AN,
Velicelebi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, mitochondrial diabetes and deafness (MIDD), an epilepsy red ragged fibre syndrome. The present sequence adenine nucleotide translocator ANT1 from human brain.
                                                                                                                                                                                                                                                                                    mitochondrial permeability transition pore component; cell sumitochondrial core component; mitochondrial related disorder; Alzheimer's disease; diabetes mellitus; hyperproliferative dis
                            Disclosure;
                                                       New nucleic acid expression constructs, useful for screening for a that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                    03-NOV-1999;
                                                                                                                                                                                                      03-NOV-2000; 2000WO-US30535
                                                                                                                                                                                                                            10-MAY-2001
                                                                                                                                                                                                                                                WO200132876-A2
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                                                                                                      AAU01198
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                                                                                                                                                               (MITO-) MITOKOR.
                                                  Eused
                                                                                                  2001-291054/30
DB; AAS05901.
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                                                                                                                                                                                                                                                                                                                                         adenine nucleotide translocator-1 (ANT-1) protein.
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                                                                                                                                                                                                                                                                                                                      adenine nucleotide translocator-1; ANT-1; MTP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                energy
                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQGIIIYRAAYEGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                6
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                            Fig
                                                                                                                                           Clevenger
                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                Davis
                                                                                                                                                                                   9905-0434354
                                                 transier
                            <u>ب</u>
                           186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                              entry)
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87.2%;
                                                                                                                                 RE,
                                                 molecule
                                                                                                                                           Wiley
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                                                                                                                                          Andreyev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8e-140;
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                                                                                                                                           ΑY,
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                                                                                                                                           Frigeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                            cell survival;
                                                                                                                                                                                                                                                                                                                     cyclophilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and myoclonic
                                                                                                                                           5
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                                                                              for agents
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The present (ANT-1) prot

sequence

proteins ar

are

human adenine nucleotide tra re mitochondrial permeability

translocator-1

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RESULT 15
AAUT0378
ID AAUT0
XX AAUT0
AC AAUT0
AC Human
DE Human
XX Human
XX Human
XX Homo
XX II-MA
XX HOMO
PF 11-MA
XX H1-MA
XX MITG
XX MITG
XX MITG
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                     Anderson CM, Davis RE, Clevenger W, W Ghosh SS, Moos WH, Pei Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                11-MAY-2001; 2001WO-US15416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adenine nucleotide translocator; ANT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenine nucleotide translocator 1 (ANT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10378 standard; Protein; 297
                                                                                                                                                                                                                                          11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200185944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitochondrial matrix protein.
                                                                                                                                                     (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPKEOGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.88;
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Pred. No. 3.8e-140;
1; Mismatches 16;
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                                                                                         Wiley SE,
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                                                                                             Miller SW,
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                                                                                                  Szabo TR;
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Search completed: August 18, 2003, 16:11:32 Job time : 85 secs

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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid (CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT (CC entries mediate the exchange of ANT synthesised in the mitochondrial (CC entries for ADP in the cytosol. (I) is useful for producing recombinant (CC aNT polypeptide by transforming a prokaryotic on eukaryotic host cell and (CC culturing the host cell. (I) is also useful for targeting a polypeptide (CC expressed as a fusion protein with the polypeptide of interest to a mitochondrial membrane, where ANT polypeptide. Is (CC expressed as a fusion protein with the polypeptide of interest. (CC expressed as a fusion protein with the polypeptide of interest. (CC expressed as a fusion protein with the polypeptide of interest. (CC expressed as a fusion protein with the polypeptide of interest. (CC expressed as a fusion protein with the polypeptide. ANT (CC expressed) and for determining the presence of an ANT polypeptide. ANT (CC expressed) ANTI, ANTO or ANTS in a biological sample and for isolating (CC expressed) and to a solid phase. Detectably labeled ANT ligand is also (CC expressed) and the polypeptide of covalently bound to a solid phase. Detectably labeled ANT ligand is also (CC expressed) and the polypeptide of the present sequence represents the amino acid sequence of human ANTI.
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Best Local S
Matches 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 44; Fig 2; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-055598/07.
DB; AAS16688.
                                                                                                                                                                             180 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM 239
                                                                                                               181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRNAM 240
                                       241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                           260;
                                                                                                                                                                                                                                                                      1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                  μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.8%; Score 1385.5; DB 23; Length 297; ilarity 87.2%; Pred. No. 3.8e-140; Conservative 21; Mismatches 16; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                             60
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 16:09:02; Search time 42 Seconds (without alignments) 682:340 Million cell updates/sec

Title: US-09-811-094-33
Sequence: 1543
Sequence: 1 MTEQAISFAKDFLAGGIAAA.....LRGMGGAFVLVLYDELKKVI 298
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ţ	ا د	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ъ	4	ω	N	1	No.	Result
ì	7//	747	747	748	750	756.5	760.5	762.5	764	766	768	769	772	778.5	943	978	993.5	1038	1039	1041	1184	1405	1409	1418	1422	1424	1454	1512	1543	Score	
4	٠,	48.4	48.4			49.0	49.3		49.5	49.6	49.8	49.8	50.0	50.5	61.1	63.4	64.4	67.3	67.3	67.5	76.7		91.3	91.9	92.2		94.2	98.0	100.0	Match	Query
007	207	386	306	386	387	306	318	305	326	313	386	322	308	307	301	339	300	300	313	313	301	298	298	298	298	298	298	298	298	Length	
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. 516000	01 65 60	S17917	T42011	S21974	S14876	T20012	A31978	S68154	T25728	XWNC	T09709	T40526	S30259	A36582	S51132	A41677	T15206	T25371	T25850	T23207	S31935	S31814	A44778	S37210	XWBO	160173	A29132	B43646	S03894	ID	
ADF, AIF COILLEL PI		Carrier	ADP, ATP carrier pr	ADP, ATP carrier pr	-	hypothetical prote	ADP, ATP carrier pr		$^{\circ}$	carrier	ADP, ATP carrier pr	transloc	ADP, ATP carrier pr		carrier	-				tical pro	н		carrier	carrier	carrier		carrier	ADP, ATP carrier pr	,ATP carrier	Description	

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61

54 B

61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120

IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120

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344.5	368	369.5	370.5	372	381	383	520.5	681.5	734.5	737.5	739.5	742	742.5	743
22.3	23.8	23.9	24.0	24.1	24.7	24.8	33.7	44.2	47.6	47.8	47.9	48.1	48.1	48.2
332	475	381	415	358	352	325	327	298	379	309	386	382	385	379
2	, ku	N	N	N	N	N	N	N	N	N	N	N	<u>-</u>	2
T47703	T50686	T51158	T48171	T45934	T01729	T04273	T51577	T24029	S21313	A24849	S14874	S33630	S29852	T04608
probable micochond Ca-dependent solut	peroxisomal Ca-dep	hypothetical prote	hypothetical prote	hypothetical prote	mitochondrial solu	hypothetical prote	ADP/ATP translocas	4	ADP, ATP carrier pr	_	ADP, ATP carrier pr		ADP, ATP carrier pr	ADP,ATP carrier pr

ALIGNMENTS

A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted <AMT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3> R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;HILE: TWO distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116 RESULT 1 S03894 밁 Q A;Molecule type: mRNA
A;Residues: 36-104,'R',106,'A',109-298 <HOU>
A;Cross-references: GB:U03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
A;Experimental source: liver 1. Mol. Biol. 206, 261-280, 1989 A; TITIE: DNA sequences of two expressed nuclear genes for human A; Reference number: S03893; MUID:89236396; PMID:2541251 A; Accession: S03894 C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: \$03894, B28116
R;Cozens, A.L.; Runswick, M.J.; Walker, J.E. ADP,ATP carrier protein T3 - human N;Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP, A; Molecule type: DNA A; Residues: 1-298 <COZ> A; Gene: GDB: ANT3; ANT3Y ; Genetics: Status: not compared with conceptual translation Query Match Best Local Similarity Matches 298; 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 100.0%; Score 1543; DB 1; ilarity 100.0%; Pred. No. 6e-129; Conservative 0; Mismatches 0; Length 298; Indels mitochondrial ADP/ATP 0; Gaps 0

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ADP,ATP carrier protein T2 - human
N;Alfornate names: mitcochondrial ADP,ATP translocase 2
N;Alfornate names: mitcochondrial ADP,ATP translocase 2
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A29192; C28116
C;Accession: A29192; C28116
R;Battini, R; Ferrari, S; Kaczmarek, L; Calabretta, B; Chen, S; Baserge
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A;Accession: B43646
A;Accession: B43646
A;Accession: preliminary
A;Accession: preliminary
A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Superfamily: ADP,ATP carrier protein repeat homology ACCPS
C;Suponain: ADP,ATP carrier protein repeat homology ACCPS
F;107-298/Domain: ADP,ATP carrier protein repeat homology ACCPS
F;207-298/Domain: ADP,ATP carrier protein repeat homology ACCPS
F;207-298/Domain: ADP,ATP carrier protein repeat homology ACCPS
     A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247 R;Houldsworth, J.; Attardi, G. Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988 A;Title: Two distinct genes for ADP/ATP translocase are expressed at the
                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-298 <BAT>
                                                                                                                                                                                                                                                                               R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R. J. Biol. Chem. 262, 4355-4559, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat A;Reference number: A29132; MUID:87166056; PMID:3031073
A;Accession: A29132
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A;Title: Two bovine genes for mitochondrial ADP/ATP tran
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Best Local S
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97.7%;
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Pred. No. 3.3e-126;
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          expressed at the mRNA level in
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C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology C; Keywords: duplication; transmembrane protein c; 5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1> E; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2> F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
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R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
B;Stile: Isolation and characterization of cDNA clones and a genomic clone encoding r
A;Reference number: 160173; MUID:94002161; PMID:8399300
A;Accession: I60173
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
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A;Accession: C28116
A;Molecule type: mRNA
A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A;Cross-references: CB:J03591; NID:9339720; PIDN:AAA36749.1; PID:9339721
A;Cxcoss-references: CB:D03591; NID:9339720; PIDN:AAA36749.1; PID:9339721
A;Experimental source: clone pHAT3
          В
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A;Molecule type: DNA
A;Residues: 1-298 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IPKEQGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
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                                                                                              1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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1 MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                                                                                                                                                           h 92.3%; Score 1424; DB 2; Length 298; Similarity 89.6%; Pred. No. 2e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                      Mismatches
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C;Comment: This protein is synthesized in the cytosol and transported into the m C;Complex: homodimer C;Complex: homodimer C;Function:

A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial AT A;Note: located in the inner mitochondrial membrane C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;110-203/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: A43646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 208-298 (-AS>
A;Residues: 208-298 (-AS>
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
R;Aquila, H.; Misra, D.; Eulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A;Title: Complete amino acid sequence of the ADP/ATP carrier A;Reference number: A03181; MUID:82188267; PMID:7076130
A;Accession: A03181
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: residue 52 may be methyllysine R; Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, Biochim. Biophys. Acta 670, 176-180, 1981 A; Title: Amino acid sequence determination of the A; Reference number: A61343; MUID:82046808; PMID:62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier:
A;Reference number: A24822; MUID:86295775; PMID:3017341
A;Accession: A24822
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R;Rasmussen, U.B.; Wohlrab, H.
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XWBO

ADP, ATP carrier protein T1 - bovine
A); Alternate names: ADP/ATP translocase
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A; Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298
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PMID:7867632
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Best Local
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GAAGATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                             MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                          92.2%;
                                                                                                                19;
                                                                                                                         Score 1422; DB 1;
Pred. No. 3.1e-118;
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QSGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKFV

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GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVS 180

VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240

VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQTVTAVAGLVSYPFDTVRRRMM

240

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A; Residues: 1-298 <LAP>
A; Cross-references: EMB
C; Genetics:
A; Gene: ANC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein C;Keywords: duplication; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>F;207-298/Domain: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S:
A; Accession: S37210
A; Status: preliminary
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S37210
ADP,ATP carrier protein T1
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                                                                                                                                                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                         IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
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Pred. No. 6
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI

VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM

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A;Map position: 4q35-4q35
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-998/Product: ADP,ATP carrier protein #status predicted <AAT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: Clone pHMANT
R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: A28116
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A;Molecule type: DNA
A;Residues: 1-298 <COZ>
A;Residues: 1-298 <COZ>
R;Neckelmann, N.; L1, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A;Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader A;Reference number: A39891; MUID:88041149; PMID:2823266
A;Accession: A39891
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J. Mol. Biol. 206, 261-280, 1989
A;Tille: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tm
A;Reference number: 603893; MUID:89236396; PMID:2541251
A;Accession: S03893
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;A;Cross: references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
A;Cross: references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
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C;Bate: 17-Mar-2000 fsequence_revision 17-Mar-2000 ftext_change 17-Mar-2000
C;Accession: A44778; S03893; A39891; A28116
R;L1, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M. J. Biol. Chem. 264, 13998-14004, 1989
A;Title: A human muscle adenine nucleotide translocator gene has four exons, is located A;Reference number: A44778
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A;Experimental source: liver
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A; Residues: 1-37 <HOU>
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;Alternate names: mitochondrial ADP,ATP translocase 1
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Best Local :
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                                                                                  121 GAAGATSLCFYYYLDFARTRLAADVGKSGTEREFRGLGDCLYKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                   IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
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A;Reference number: S31935
A;Accession: S31935
A;Accession: Forlininary
A;Accession: Forlininary
A;Molecule type: DNA
C;Accession: C;BEA>
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
                                                                                                                                                                                                                                                                                            ADP,ATP carrier protein - African malaria mosquito
(;Species: Anopheles gambiae (African malaria mosquito)
(;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
(;Accession: S31935; S31936
(;Accession: S1935; S31936
(;Accession: C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A;Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X70847
A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; transmembrane protein repeat homology <ACP1>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Molecule type: mRNA
A;Residues: 1-298 <COS>
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N;Alternate names: adenine nucleotide translocase
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C;Accession: S31814
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Best Local :
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Similarity 89.2%; Pred. No. 9.8e-117;
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RESULT 10
T23207

Pypothetical protein K01H12.2 - Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data A; Reference number: Z19707 A; Accession: T23207
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A;Experimental source: clone K01H12
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-313 <WIL>
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Best Local Sim
Matches 231;
                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T23207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTEQA--ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCI 58
                                                                                                                          LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY 187
                                                                                                                                                                                 LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                       VSVQGIIIYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                                                                                   AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGGAAGATSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFN
            ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                   RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKG
                                                      RAAYFGMFDTAKMVFTADGKKLNFFAAWATAQVVTVGSGIISYPWDTVRRRMMMQSGRK-
                                                                                                            LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP, ATP
ADP, ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.78;
77.08;
                                                                                                                                                                                                                                                                              67.5%; Score 1041; DB 2; 70.9%; Pred. No. 1.7e-84; tive 29; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carrier protein repeat homology <ACP2>
carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library, December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1184; DB 1;
Pred. No. 3.6e-97;
23; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995
                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                        Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 301;
                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                              Gaps
                                                                                246
                                                                                                                                                                   144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                            203
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-300 <WIL>
A; Cross-references: EMBL: Z82059; PIDN: CAB04874.1; GSPDB: GN00021; CESP: T27E9.1
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
T25371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T01B11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
                                                                                                                                                                                                                                                                                             hypothetical protein T27E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t/C;Accession: T25371 R;Lloyd, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4 A;Experimental source: strain Bristol N2; clone T01B11 C;Genetics:
                                                                                                                                                                                                                       submitted to the EMBL Data
A; Reference number: Z20024
A; Accession: T25371
A; Status: preliminary; tran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: The sequence
A; Reference number: Z20099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, December 1996 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T25850
R;Geisel, C.; Stellyes,
                                                                   A; Map position: 3
A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-313 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:T01B11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T25850
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                      263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 67.3%;
Similarity 70.9%;
07; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAAYEGMEDTAKMVETADGKKLNEFAAMAIAQVVTVGSGILSYPWDTVRRRMMMQSGRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAAYFGVYDTAKGMI-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                              115/2 carrier protein; ADP,ATP carrier protein repeat
                                                                                                                                                                                                                           translated
                67.3%;
69.2%;
                                                                                                                                                                                                                                                                             Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1039; DB 2;
Pred. No. 2.6e-84;
Score 1038; DB Pred. No. 3e-84; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                               November 1996
                                                                                                                                                                                                                                                                                                                               15-Oct-1999 #text_change 11-Jan-2000
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                                                                                                                                                                                                                           GB/EMBL/DDBJ
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                                 DB 2;
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                                   Length 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
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                                                                   homology
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Best Local

Similarity

Conservative

37;

49;

4;

Gaps

ω

Matches 202;

В

Qy Дb Ş B Ş

밁 QΥ B

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R;Le, T.; Weinstock, L.; Rifkin, L.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid W02D3.
A;Reference number: Z18308
A;Accession: T1526
A;Accession: T1526
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-300 <LET>
A;Residues: 1-300 <LET>
A;Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GN
A;Experimental source: strain Bristol N2; clone W02D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:W02D3.6
A;Map position: 1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F;9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
T15206
T15206
hypothetical protein W02D3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #to
C;Date: 20-Sep-1999 #to
C;Date: 7-; Weinstock, L.; Rifkin, L.
R;Le, T.; Weinstock, L.; Rifkin, L.
            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                   238 MMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VSVQGIIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 ICFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY 187
                                                                                                                         300 I 300
                                                                                                                                                                                              298 I 298
                                                                                                                                                                                                                                                               242 MMMQSGRK--DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQHL
                                                                                                                                                                                                                                                                                                                                                                                                         182 VSVQGIIIYRAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ARVPKEQGYAAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 AALWRGNLANVIRYFPTQAMNFAFKDTYKAIFLEGLDKKKDFWKFFAGNLASGGAAGATS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAAYFGMFDTAKMVFASDGQKLNFFAAWGIAQVVTVGSGILSYPWDTVRRRMMMQSGRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCFVYPLDFARTRLAADIGKA-NDREFKGLADCLIKIVKSDGPIGLYRGFFVSVQGIIIY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.4%; Score 993.5; DB 2; Length 300; 64.8%; Pred. No. 2.6e-80; tive 40; Mismatches 59; Indels 7
                                                                                                                                                                                                                            RESULT 15

S51132

ADP, ATP carrier protein - malaria parasite (Plasmodium falciparum)

ADP, ATP carrier protein - malaria parasite (Plasmodium falciparum)

N;Alternate names: ADP/ATP transporter

C;Species: Plasmodium falciparum
C;Date: 07-May-1955 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C;Accession: $68993; S51132

K;HatLin, I; Jaurequiberry, G.

Eur. J. Blochem. 228, 86-91, 1995

A;Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the human ma
A;Reference number: $68993; MUID:95188918; PMID:7883016

A;Reference number: $68993; MUID:95188918; PMID:7883016

A;Accession: $68993

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-301 <4MI:
A;Cross-references: EMBL:X83551; NID:9623334; PIDN:CAA58541.1; PID:9623335
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology <ACP1>
F;61-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA1677
ADP, ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: A41677
C;Accession: A41677
R;Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and the glycera
A;Title: Glucose increases the expression of the ATP/ADP translocator and the glycera
A;Title: Glucose increases in the expression of the ATP/ADP translocator and the glycera
A;Title: Glucose increases in A1677
A;Accession: A41677; MUID:92084708; PMID:1748677
A;Accession: A41677
A;Accession: A41677
A;Accession: A41677
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-339 <HILD
A;Residues: 1-339 <HILD
A;Cross-references: GB:M76669; NID:9516596; PIDN:AAA33027.1; PID:9516597
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology <ACP1>
E;38-134/Domain: ADP,ATP carrier protein repeat homology <ACP1>
E;144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                           ğ
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                                                                                                                                                                                 Query Match
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Best Local :
                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 GRÇADIMYTGYYDCWRRIFRDEGGRAFFKÇAWSNYLRGMGGAFYLVLYDELKKVI 298
GRÇADIMYTGYYDCWRRIFRDEGGRAFFKÇAWSNYLRGMGGAFYLVLYDELKKVI 298
277 ---GGERQYNGTICCWRKVAQQEGMKAFFKÇAWSNYLRGAGGAFYLYLYDEIKKFI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 IIIYRAAYEGUYDTAKGML-PDPKMTHIVVSKMIAQTVTAVARGVVSYYPDTVRRRMMOS 242
11 IIYRAAYEGUYDTAKGML-PDPKMTHIVVSKMIAQTVTAVARGVVSYYPDTVRRRMMOS 246
217 IIVYRGAYEGUYDTAKGYLFKDERTANFFAKWAVAQAVTAGAGYLSYPPDTVRRRLMMOS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 GAGSLLIVYPLDFARTRLAADVG-SGKSREFTGLVDCLSKVVKRGGPMALYQGFGVSVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
                                                                                                                    183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 EQGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLFPKYSPK-TDFWRFFVVNLASGGLA 157
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7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAAD--KQYKGIVDCIVRIPKE 64
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98; Conservative
                                                                                                                                                   Similarity
                                                                                                                61.1%; Score 943; DB 2; Length 301; llarity 61.8%; Pred. No. 7.6e-76; Conservative 45; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.4%; Score 978; DB 2; Length 339; 66.9%; Pred. No. 7.1e-79;
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245	186 IVYRGSYFGLYDSAKALLFTUDKUTUIVLKWAVAOSVTILAGLISYPFDTVRRRMMMSG 245	186	
243	185 IIYRAAYEGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMQSG 243	185	νQ
185	127 AISLLIVYPLDFARTRLASDIGK-GKDRQFTGLFDCLAKIYKQTGLLSLYSGFGVSVTGI 185	127	₽ B
184	125 ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184	125	Qy
126	68 QGVLSLWRGNVANVIRYFPTQAFNFAFKDYFKNIF-PRYDQNTDFSKFFCVNILSGATAG 126	68	Db
124	03 OGVISSEWRGNIANVIRTEFTQALKEAFURTRQIFLGGVDRHTQFWRTFAGNLASGGAAG 124		: 5
		<u> </u>	?
67	8 NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRVSKE 67		

Search completed: August 18, 2003, 16:14:34 Job time : 43 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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1543
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p32007 bos taurus
p35141 homo sapien
Q09073 rattus norv
p51881 mus musculu
Q05962 rattus norv
p48962 mus musculu
p02722 bos taurus
p12235 homo sapien
Q26365 drosophila
Q27238 anopheles
p31692 chlorella k
p18238 saccharomyc
p27080 chlamydomon
Q09188 schizosacch
Q22342 gossyplum h
p02723 neurospora
p49382 kluyveromyc
p18239 saccharomyc
p18239 saccharomyc
p18239 saccharomyc
p18239 salanum tub
p31167 zea mays (m
p31167 zea mays (m
p31167 arabidopsis
Q41629 triticum ae
p27081 solanum tub
p04710 saccharomyc
Q41630 triticum ae
Q19529 caenorhabdi
Q01988 bos taurus
Q99297 saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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45	44	43	42	41	40	39	38	37	36	35	34
265	265	270	272	280	282.5	284	285	286	287.5	289.5	295
17.2	17.2	17.5	17.6	18.1	18.3	18.4	18.5	18.5	18.6	18.8	19.1
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ALIGNMENTS

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SEQUENCE OF 36-298 FROM N.A. TISSUE-Liver; MEDLINE-88124845; PubMed-2829183; Houldsworth J., Attardi G.; "Two distinct genes for ADP/ATP translocase are expressed at the mrna	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	ט	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Touchman J.W., Green E.D., Dickson M.C.,	Hulyk S.	S., Carninci P., Prange C., , Abramson R.D., Mullahy S.	HOPKING K.F., WOTGER H., MOOTE T., MAX S.I., WANG J., HSIEN F., DIATCHENKO L., WARUSINE K., FARMER A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	T		SEQUENCE FROM N.A. TISSUE-Brain, Cervix, Eye, and Lung;	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,	7. Mol. Biol. 206:261-280(1989).	Cózens A.L., Runswick M.J., Walker J.E.; **DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.**;	12-1 SEQUENCE FROM N.A. MEDLINE-89236396; PubMed-2541251;	F 1 Linux CCO,	nomo sapiens (numan). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Entheria: Drimatos: Catarrhin; Cominidas: Como	nine nucleotide translocator 3) (ANT 3). A6 OR ANT3.	(Rel. 42, rier prote	12, Creat	AN 3_HUM

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Best Local
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EMBL; AV007135; AA601998.1; -.
EMBL; BC007295; AAH07295.1; -.
EMBL; BC007295; AAH07295.1; -.
EMBL; BC007850; AAH07850.1; -.
EMBL; BC008737; AAH08737.1; -.
EMBL; BC008935; AAH08935.1; -.
EMBL; BC008935; AAH08935.1; -.
EMBL; BC014775; AAH14775.1; -.
PIR; S03894; S03894.
Genew; HGNC:10992; SLC25A6.
MIM; 300151; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCOUPLING.
PROSITE; PS00215; MITOCH_CARRIE
Mitochondrion; Inner membrane;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      level in
Proc. Nat
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InterPro;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005744; C:mitochondrial inner membrane translocase GO:0005471; F:AFF/ADP antiporter activity; NAS. GO:000684; P:AFF/ADP exchange; TAS. erpro; IPR002067; Mit_uncoupling. erpro; IPR0020306; Mit_uncoupling. erpro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBURITAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
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181
                                  181
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                                                                                                                                                                                                                                                                                            Similarity
                    VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                        MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
  VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
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S -> F (IN REF. 3; AAH147;
18534E9F0E49672F CRC64;
                                                                                                                                                                                                                                                                                          Score 1543; DB 1;
Pred. No. 3.6e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (POTENTIAL).
2 (POTENTIAL).
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O1-JUL-1993 (Rel. 26, Last s
16-OCT-2001 (Rel. 40, Last a
ADP,ATP carrier protein, iso
nucleotide translocator 3) (
SLC25A6 OR ANT3
                                                                                                                    MITOCHONDITION; INNE
MULTIGENE family.
TRANSMEM 12
TRANSMEM 73
TRANSMEM 117
TRANSMEM 117
TRANSMEM 274
TRANSMEM 274
TRANSMEM 273
REPEAT 273
REPEAT 112
REPEAT 209
SEQUENCE 298 AA;
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P32007;
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Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
Biochemistry 28:866-873(1989).
-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; (
Mammalia; Eutheria;
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PIR; B43646; B43646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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SIMILARITY: Belongs to the mitochondrial carrier family.
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SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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ipR002030; Mit_uncoupling.
ipR001993; Mitoch_carrier.
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26, Last sequence update)
40, Last annotation update)
rotein, isoform T2 (ADP/ATP translocase ocator 3) (ANT 3).
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                                                                98.0%;
97.7%;
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                                                                   Score 1512;
Pred. No. 1
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P05141; 043350;
13-AUG-1987 (Rel. 05, Created)
01-OCT-1994 (Rel. 30, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation upda
ADP,ATP carrier protein, fibroblast iso;
(Adenine nucleotide translocator 2) (AM: SLC25A5 OR ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISUE--lacenta;

MEDLINE-90375457; PubMed-2168878;

MEDLINE-90375457; PubMed-2168878;

Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga F

"The human fibroblast adenine nucleotide translocator cloning and sequence.";

cloning and sequence.";

J. Biol. Chem. 265:16060-16063(1990).
                                                                                                                                                                                                                                                                                                                         Submitted [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-87166056; PubMed-3031073;
Accommondation of the common of the common
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Proc.
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J. Biol. Chem. 262:4355-4358(1987)
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Mammalia; Eutheria;
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growth-regulated.";
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                                                                                  FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral me
                      DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carr
                                                                  inner membrane
                                                                                                                                              distinct genes for ADP/ATP translocase are 1 in adult human liver.";
. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
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A.A., Schlessinger D., Chen E.Y.;
(JUN-1996) to the EMBL/GenBank/DDBJ
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n E.Y.;
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RESULT 4
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GO; GO:0015207; F:adenine transporter activity; TAS.
GO; GO:0006832; P:small molecule transport; TAS.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
PF00153; Mitoch_carrier.
PF00153; Mitoch_carrier.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRIER; 3.
PRINTS; PR00784; MITOCH_CARRIER; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; M57424; AAA51737.1; -.
; J02683; AAA35579.1; -.
; L78810; AAB39266.1; -.
; AC004000; AAB96347.1; -.
                                                                                                                                   181
                                                                                                                                                        181
                                                                                                                                                                                 121
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                                                                                     241
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                                                                                  GAAGATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                         IPKEQGVLSEWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                          MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
||:|:|||||||||:||:||
MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                             IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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162
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91
134
195
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291
111
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66
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162
32895
                                                                                                                                                                                                                                                                                                                                      94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane;
                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                          Score 1463; D
Pred. No. 3.8e
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        V -> L (IN REF. 2).
3 -> E (IN REF. 2).
R -> L (IN REF. 4 A).
V -> G (IN REF. 5).
F973C3AED92C49D3 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                          .8e-121;
ies 8;
                                                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                   296
                                                                                                         296
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(Rel. 31, Created)

STANDARD;

PRT;

298

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Best Local S
Matches 272
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MEDLINE-94002161; PubMed-8399300;

Shinohara Y, Kamida M, Yamazaki N, Terada H.;

Shinohara Y, Kamida M, Yamazaki N, Terada H.;

"Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator.";

Blochim. Blophys. Acta 1152:192-196(1993).

1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

1- SUBUNIT: HOMODIME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
ADP_ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
(Adenine nucleotide translocator 2) (ANT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
PRINTS;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D12771; BAA02238.1; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
- I- SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inner membrane.
-!- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLC25A5 OR ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKELETAL MUSCLE
                                                                                                                                                                                                                272;
                                                                                         61
                                                                                                                     61
                                                                                                                                                   μ
                                                                                                                                                                    1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00784; MTUNCOUPLING.; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                Similarity
                                                                                                         IPKEQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASG
                                               GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                           IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                    MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
 VQGTTTYRAAYFGVYDTAKGMLPDPKNTHTVVSWMTAQTVTAVAGVVSYPFDTVRRRMM
                               GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
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73
117
176
214
273
273
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Inner membrane;
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134
195
231
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                                                                                                                                                                                                                                                                           32901 MW;
                                                                                                                                                                                                                                94.0%;
91.9%;
                                                                                                                                                                                                                15;
                                                                                                                                                                                                                              Score 1451;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                           6A59204B987EFE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                4.3e-120;
                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                              Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEART, LIVER AND
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                  Gaps
                                   180
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DE PROPERTO DE LA COMPANSION DE LA COMPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                    EMBL; U27316; AAC52838.1; --
EMBL; U10404; AAA19009.1; --
EMBL; X70847; CAA50196.1; --
EMBL; AF240003; AAF64471.1; --
MGD; MGI:1353496; S1c25a5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
"Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
Gene 254:57-66(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97059403; PubMed-8903724;
Ellison J.W., Li X., Francke U.,
"Rapid evolution of human pseudoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Costet P., Laplace C.;
Submitted (FEB-1993) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-129/SV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thesis (1995), University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMOdimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PubMed=10974536;
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pseudoautosomal genes and their mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              П.ж.
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IPR002067; Mit_carrier

AAF64471.1; -.

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Best Local S
Matches 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene family.
TRANSMEM 12
TRANSMEM 73
TRANSMEM 117
TRANSMEM 176
TRANSMEM 214
TRANSMEM 273
                                                                                                                                                                                           Q05962;

Q1-FEB-1994 (Rel. 28, Crea

Q1-FEB-1994 (Rel. 28, Last

16-OCT-2001 (Rel. 40, Last

ADP,ATP carrier protein, h

translocase 1) (Adenine nu
                         STRAIN-Sprague-Dawley, and Wistar; TISSUE-Heart, and Liver; MEDLINE-94002161; PubMed-8399300; Shinohara Y., Kamida M., Yamazaki N., Terada H.; "Isolation and characterization of cDNA clones and a genomi encoding rat mitochondrial adenine nucleotide translocator. Blochim. Biophys. Acta 1152:192-196(1993).

-I-FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS MITOCHONDRIAL INNER MEMBRANE.

-I-SUBURIT: Homodimer.
-I-SUBURIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion;
            +
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        ADT1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                     SLC25A4 OR ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
          Inner membrane.
TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                          norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
                                                                                                                                                                                                                                                                                                                                           MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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IPR001993; Mitoch_carrier
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Mammalia; Eutheria; NCBI_TaxID=10090;

Craniata; Vertebrata; Euteleostomi;

isoform T1 (ANT 1)

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Muridae;

Murinae;

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PA8962; 062164;

101-FEB-1996 (Rel. 33, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

16-SEP-2003 (Rel. 42, Last annotation update)

17-SEP-2003 (Rel. 42, Last annotation update)

18-SEP-2003 (Rel. 42, Last annotation update)

19-SEP-2003 (Rel. 42, Last annotation update)

19-SEP-2003 (Rel. 42, Last annotation update)

19-SEP-2003 (Rel. 42, Last annotation update)

20-SEP-2003 
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PRINTS; PR00784; MITOCH_CARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
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InterPro; IPR001993; Mitc
Pfam; PF00153; Mitc_carr;
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InterPro; IPR002067;
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D12770; BAA02237.1;
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; Mit_uncoupling.
; Mitoch_carrier.
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MGD: MGI:1353495; Slc25a4.

InterPro: IPR0020507; Mit_carrier.

InterPro: IPR002030; Mit_uncoupling.

InterPro: IPR001939; Mitcoh_carrier.

Pfam; PF00153; mitc_carr; 3.

PRINTS; PR00784; MITOCCHERR.

PRINTS; PR00784; MITOCH_CARRIER.

PRINTS; PR00785; MITOCH_CARRIER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ellison J.W., Li X., Francke U., Shapiro 1 "Rapid evolution of human pseudoautosomal homologs.";
                                                                                                                                                                                                                                                                      EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-97059403; PubMed-8903724;
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SEQUENCE FROM N.A.
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Inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carrier family.
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X74510; CAA52616.1; -.
AF240002; AAF64470.1; -.
BC003791; AAH03791.1; -.
BC026925; AAH26925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome 7:25-30(1996).
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Multigene family.

TRANSMEM 12

TRANSMEM 73

TRANSMEM 176

TRANSMEM 176

TRANSMEM 214

TRANSMEM 273

REPEAT 11

REPEAT 11

REPEAT 10

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P02722;
21-JUL-1986
01-JUL-1993
16-OCT-2001
                                                                                                                                  SEQUENCE.

SEQUENCE.

MEDILINE-82188267; PubMed-7076130;

Aquila H., Misra D., Eulitz M., Klingenberg M.;

"Complete amino acid sequence of the ADP/ATP carrie
mitochondria.";

Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).

[3]
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01-UUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (AD
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                                                                                                                                                                                                                                                                                                                                                                                               Powell S.J., Medd S.M., Runswick M.J.,
"Two bowine genes for mitochondrial Abl
differences in various tissues.";
Blochemistry 28:866-873(1989).
SEQUENCE OF 207-297 FROM N.A.
MEDLINE-86295775; PubMed-3017341;
Rasmussen U.B., Wohlrab H.;
"Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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Pred. No. 3.4e-117;
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3A849FEAB0981462 CRC64;
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                                                                                                                                                                                                                                             Klingenberg M.;
f the ADP/ATP carrier
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ADP/ATP translocase
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PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MIUNCOUPLING.
PROSITE; PS00215; MITOCH CARRIER;
Mitochondrion; Inner membrane; Rej
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InterPro: IPR002030; Mit_uncoupling.
InterPro: IPR001993; Mitoch_carrier.
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, M24102; AAA30768.1;
A43646; XWBO.
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                                                          SGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKFV
                                                                    SGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                 QGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQTVTAVAGLVSYPFDTVRRRWMQ
                                                                                                            QGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRWMQ
                                                                                                                                         AAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVSV
                                                                                                                                                  AAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
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70mmun. 138:850-857(1986)
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METHYLATION
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RX MEDLINE=22388257; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McEwan R.J., Malek J.A., Gunaratine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-88041149; PubMed-2823266;

MEDLINE-88041149; PubMed-2823266;

Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;

"CDNA sequence of a human skeletal muscle ADP/ATP translocator:

of a leader peptide, divergence from a fibroblast translocator
and coevolution with mitochondrial DNA genes.";

and coevolution with mitochondrial DNA genes.";

and coevolution with mitochondrial DNA genes.";
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J. Mol.
[2]
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
SLC25A4 OR ANT1.
Kaukonen J., Juselius J.K., Tiranti V., I
Comi G.P., Keranen J., Peltonen L., Suome
"Role of adenine nucleotide translocator
Science 289:782-785(2000).
-!- FUNCTION: CATALYZES THE EXCHANGE OF 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89236396; PubMed=2541251; MEDLINE-89236396; PubMed=2541251; Walker J. Walker J.
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Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace
"A human muscle adenine nucleotide translocator gene has
is located on chromosome 4, and is differentially express
J. Biol. Chem. 264:13998-14004(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           VARIANTS PEO PRO-114 AND MET-289
MEDLINE-20385067; PubMed-1092654
                                                                                                                                                                    Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are level in adult human liver.";
                                                                                                                                                                                                                              MEDLINE=88124845; PubMed=2829183
                                                                                                                                                                                                                                                                    SEQUENCE OF 1-37
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                                                                                             PubMed=10926541;
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                                                                                                                                                                                                                                                                      N.A.
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                                                     V., Kyttala
Suomalainen
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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51786.1; -.
EMBL; BC008664; AAH08664.1; -.
EMBL; BC008664; AAH08664.1; -.
PIR; A44778; A44778.
Genew; HGNC:10990; SLC25A4.
MIM; 103220; -.
MIM; 103220; -.
MIM; 10320; -.
MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr; 3.
PRINTS; PR0926; MITOCARRIER.
PRINTS; PR00784; MUDUCOUPLING.
PROSITE; PS00215; MITOCH_CARRIE
Mitochondrion; Inner membrane;
Multigene family; Disease mutat
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial mypathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.

SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0006832; P:small molecule transport; erPro; IPR002067; Mit_carrier. erPro; IPR002030; Mit_uncoupling. erPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005687; C:integral to plasma membrane; TAS. GO:0005739; C:mitochondrion; TAS. GO:0015207; F:adenine transporter activity; TAS. GO:0006091; P:energy pathways; TAS. GO:0000002; P:mitochondrial genome maintenance; TAS.
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SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
61
                                                                                                                                                                                                                                  Similarity
                  IPKEQGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                        MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                          16
147
227
298 AA;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCH_CARRIER; 3
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mutation.
                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                  A -> P (IN PEO).

/FTId=VAR_012111.

V -> M (IN PEO).

/FTId=VAR_012112.

G -> A (IN REF. 3).

KGA -> RR (IN REF. 3).

V -> L (IN REF. 3).
                                                                                                                                                                                                                            Score 1409; DB 1;
Pred. No. 2.1e-116
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(POTENTIAL).
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Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A candidatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A candidatides P.G., Scherer S.E., Holt P.W., Hoskins R.A., Galle R.F.,
A candidatidation G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Basun A., Baxendale J., Bayraktarogin L., Beasley E.M.,
Basun R.M., Basun A., Bayraktarogin L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Berriera S., Fleischmann W.,
Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Cherry C., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyman C.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyman C.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyman C.,
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15-7UL-1998 (Rel. 36, Created)
128-FEB-2003 (Rel. 41, Last sequence update)
15-SED-2003 (Rel. 42, Last annotation update)
2 ADP,ATP carrier protein (ADP/ATP translocase) (Adeni
2 translocator) (ANT) (Stress sensitive B protein).
N SESB OR A/A-T OR CG16944.
2 ENKaryota; Metazoa; Arthropoda; Hexapoda; Insecta; P
C Neoptera; Endopterygota; Diptera; Brachycera; Muscom
C Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louvi A., Tsitilou S.G.;
"A CDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases.";
J. Mol. Evol. 35:44-50(1992).
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Submitted (JAN-1997) to
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"Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila.";
Experientia 50:749-762(1994).
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MEDLINE-94350065; PubMed-7520869;
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Brachycera; Muscomorpha;
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Merkulov G., Milshina N.V., Mobarry C., McLeod M.P., McIson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., McTis J., Mesherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Niusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhan Q.A.,
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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.",
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   EMBL; $43651; AAB23114.1; -.

EMBL; $71762; AAB31734.3; -.

EMBL; Y10618; CAA71628.1; -.

EMBL; RE003404; AAP47957.1; -.

EMBL; AV060970; AAL28526.1; -.

EMBL; AV070894; AAL48516.1; -.

EMBL; AV070894; AAL48516.1; -.

F1yBase; FB9n0003360; sesB.

GO; GO:0005743; C:mitochondrial transport; IM

InterPro; IPR001093; Mitochondrial transport; IM

InterPro; IPR001993; Mitochondrial transport; IM

PRINTS; PR00153; mito_carrier.

PRINTS; PR00153; mito_carrier.

PRINTS; PR00936; MITOCARRIER.
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"A Drosophila full-length cDNA resource.";

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Berkeley; TISSUE-Larva, Ovary, and MEDLINE-22426066; PubMed-12537569; Stapleton M., Carlson J.W., Brokstein P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Berkeley; T
MEDLINE-22426066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane (By similarity).
DOMAIN: Composed of three homologous domains.
SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Catalyzes the exchange of ADP mitochondrial inner membrane.
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane
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Q27238;
                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@fisb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
PROSITE; PS00215; MITOCH_CARRIER; 3.
MITOCHONDRION; Inner membrane; Repeat; Transmembrane;
TRANSMEM 14 31 1 [POTENTIAL].
TRANSMEM 75 93 2 [POTENTIAL].
TRANSMEM 119 136 3 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insect Mol. Biol. 3:35-40(1994).
-- FUNCTION: CATALYZES THE EXCHANGE OF MITOCHONDRIAL INNER MEMBRANE.
-- SUBUNIT: Homodimer (By similarity)
-- SUBCELLULAR LOCATION: Integral mem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae (African malaria mosquito). Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins Neoptera; Endopterygota; Diptera; Nematocera; NCBI_TaxID-7165;
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                                                                                                                                                           EMBL; L11618; AAB04104.1; -.
EMBL; L11617; AAB04105.1; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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DOMAIN: COMPOSED OF THREE HOMOLOGOUS
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Best Local S
Matches 233
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-92084708; PubMed-1748677;

Hilgarth C., Sauer N., Tanner W.;

"Glucose increases the expression of the ATP/ADP translocator and iglyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";

J. Biol. Chem. 266:24044-24047(1991).

"I FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

"I SUBCULTULAR LOCATION: Integral membrane protein. Mitochondrial
             EMBL; M76669; AAA33027.1; -.
PIR; A41677; A41677.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr;
Pfam; PF00153; MITO_CARRIER.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlorella kessieri.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
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SIMILARITY: Belongs to the mitochondrial carrier family.
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233; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTEQA--ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCI
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MITOCH_CARRIER;
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5 (POTENTIAL).
6 (POTENTIAL).
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ADC APT3_YEASY
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Best Local :
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TRANSMEM 45
TRANSMEM 103
TRANSMEM 153
TRANSMEM 203
TRANSMEM 241
TRANSMEM 304
                                                                                        Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
Submitted (AUG-1994) to the EMBL/GenBank/DDJ databases.
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADD AND ATD ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
-i- SUBURIT: HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
ADP.ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ATT 3).
AAC3 OR YBR085W OR YBR0753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
ICBI_TaxID=4932;
                                                                                                                                                                                                                                                       SEQUENCE OF 38-307 FROM N.A. STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                               Andre B., Cziepluch C., Hein C., Vissers S.;
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILINE-90324269; PubMed-2165073;
KOlarov J., Kolarova N., Nelson N.;
"A third ADP/ATP translocator gene in yeast.";
J. Biol. Chem. 265:12711-12716(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADT3_YEAST
P18238;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
inner membrane.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: Belongs to the mitochondrial carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GRKGADIMYTGTYDCWRRIFRDEGGKAFFKGAWSNYLRGMGGAFYLVLYDELKKVI 298
277 ---GGERQYNGTIDCWRRVAQDGMKAFFKGAWSNYLRGAGGAFYLVLYDEIKKFI 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG
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36686 MW;
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Pred. No. 1
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Best Local S
Matches 161
                                                                                                                                                                                               ADT_CHLRE STANDARD; PRT; P77080; O1-AUG-1992 (Rel. 23, Created) O1-AUG-1992 (Rel. 23, Last sequence O1-CCT-1994 (Rel. 30, Last annotat: ADP,ATP carrier protein (ADP/ATP titranslocator) (ANT).
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SGD;
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                                                                                                                   Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorop
Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER;
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                                                        SEQUENCE FROM N.A.
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Multigene fami
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InterPro; iPR001993; Mitoch_carrier.
                     MEDLINE-93204887;
                                       STRAIN-FUD44-R2;
                                                                                                  NCBI_TaxID=3055;
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GO:0005471; F:ATP/ADP antiporte:
GO:0006854; P:ATP/ADP exchange;
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Pred. No. 4.5e
5; Mismatches
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(POTENTIAL).
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                                                                                                                                        Chlorophyceae;
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\.5e-61;
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the European Bioinformatics Institute. The
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure, evolution and expression translocator gene from Chlamydomonas Mol. Gen. Genet. 237:134-144(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S30259; S30259.
InterPro; IPR002067;
InterPro; IPR001993;
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-!- FUNCTION: CATALYZES THE EXCHANGE
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion;
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SIMILARITY: Belongs to the mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSVSVQGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIV
                                                                                                                                                                                                                                                                                                                                                     RRMMMTS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTVREEGFGSLWRGNTANVIRYFPTQALNFAFKDKFKRMF--GFNKDKEYWKWFAGNMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLAS
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(Rel. 35, Last sequence up
(Rel. 41, Last annotation
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5; Mismatches
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Pred. No. 1
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Transport.
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1.7e-60;
hes 81;
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ADP, ATP carrier protein translocator) (ANT).

(ADP/ATP translocase)

(Adenine nucleotide

update)

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RX MEDLINe-21848401; PubMed=11859360;
RA MEDLINE-21848401; PubMed=11859360;
RA Squuros J., Peat N., Hayles J., Basham D., Bowman S.,
RA Squuros J., Peat N., Hayles J., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Holroyd S., Hornaby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Gentles Y., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA McOney P., Moule S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Wothylor K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moest D., Mutler S.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moest D., Wottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., McCombie W.R., Paulsen I., Potashkin J.,
RA Spakovski G.V., Ussery D., Barrell B.G., Murse P.,
Ra Spakovski G.V., Ussery D., Barrell B.G., Nurse P.,
Ra Spakovski G.V., Ussery D., Barrell B.G., Nurse P.,
Ra Spakovski G.V., Ussery D., Barrell B.G., Nurse P.,
Ra Spakovski G.V., Barrell B.G., Nurse P.,
Ra Spakovski G. W., Paulsen I., Potashkin J.,
Ra Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.;

"Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Gene 171:113-117(1996).

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-972;
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Schizosaccharomycetales;
Schizosaccharomyces.
                                                            GeneDB_SPombe; SPBC530.10c; ...
InterPro; IPR0012067; Mit_carrier.
InterPro; IPR001293; Mitoch_carrier.
InterPro; IPR00133; mito_carr; 3.
PRINTS; PR00125; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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                                                                                                                                                                         EMBL; AL023634; CAA:
PIR; T40526; T40526
GeneDB_SPombe; SPBC
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TRANSMEM 2
  Inner membrane; Repeat; Transmembrane; 8 48 1 (POTENTIAL).
3 111 2 (POTENTIAL).
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Ascomycota; Schizosaccharomycetes;
etales; Schizosaccharomycetaceae;
                                                  Transport.
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263 TSGEA---VKYSSSFECGRQILAKEGARSFFKGAGANILRGVAGAGVLSIYDQVQ 314
                                             203 VGIVVYRGLYFGMYDTLKPVVLVGPLEGNFLASFLLGWAVTTGSGVASYPLDTIRRRMM
                                                             182 QGIIIYRAAYFGYYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                           124 GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
                      241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                            143 GAASLLFVYSLDYARTRLANDAKSAKKGGERQFNGLVDVYRKTYRSDGLRGLYRGFGPSV
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                                                                                                                                                                                                         7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADK---QYKGIVDCIVRIPK 63
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                                                                                                                                          TFFFDFMMGGVSAAVSKTAAAPIERVKLLIQNQ--DEMIRAGRLSHRYKGIGECFKRTAA
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35020 MW;
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4 (POTENTIAL).
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6 (POTENTIAL).
8AC3D16A40F41AFC CRC64;
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Search completed: August 18, 2003, 16:12:02 Job time : 25 secs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
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sp_bacteria:*
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sp_unclassified:*
sp_rvirus:*
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OBaym3 gallus gall
OBSqh5 bos taurus
OBjhiO brachydanio
O46373 oryctolagus
O959m9 xenopus lae
OBbvi9 mus musculu
O9prh1 rana rugosa
O9yic4 rana rugosa
                                                                                                                                                                                                                                                                     Description
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	48.5	48.8	•	49.2	49.3	49.5	•		53.6	•	59.9	60.4	60.7	61.1	61.2	61.2	61.3	61.4	63.1	64.4	64.4	64.5	67.2	•	67.3	67.5	72.5	73.7	75.1
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121 GAAGATSLCFVYPLDFARTRLAADVGKAGADREFSGLGDCLVKITKSDGLRGLYQGFNVS 180	121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180	61 IPKEQGYLSFWRGNLANVIRYEPTQALNFAFKDKYKQVFLGGVDKHTQFWRYFAGNLASG 120	61 IPKEQGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120	1 MADQAISFLKDFLARGVAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIIDCVVR 60	1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60	Query Match 95.5%; Score 1474; DB 13; Length 298; Best Local Similarity 93.0%; Pred. No. 2.5e-125; Matches 277; Conservative 14; Mismatches 7; Indels 0; Gaps 0;	EMBL; AB088686; BAC15533.1; SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;	FEBS Lett. 0:0-0(2002).	"Cold-induced mitochondrial uncoupling and expression of chicken UCP	Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;	SEQUENCE FROM N.A.	(1) (1)	Gallus.	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Gallus gallus (Chicken).	AVANT.	rel.	(TrEMBLiel. 23,	:-2003 (TrEMBLrel.		OBAYM3 PRELIMINARY: PRT: 298 AA.

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Indels Length 298;

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120

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Q8SQH5;
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamazaki N., Shinohara Y., Tanida K., Terada H., Structural properties of mammalian mitochondrial ADP/ATP carriers: identification of possible amino acids that determine functional differences in its isoforms.", Mitochondrion 1:371-379(2002).
EMBL: AUU05433; BAB84073.1;
EMBL: AUU05433; BAB84073.1;
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Ol-JUN-2002 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adenine nucleotide translocator 2.
                OBJHIO;
01-OCT-2002 (TIEMBLIEL. 22, Created)
01-OCT-2002 (TIEMBLIEL. 22, Last sequence update)
01-MAR-2003 (TIEMBLIEL. 23, Last annotation update)
Solute carrier family 25 member 5 protein.
SLC25A5.
SLC25A5.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR001993; mitoch_carrier. pfam; pr00153; mito_carr; 3. pr05ITE; p800215; mITOCH_CARRIER; 3. SEQUENCE 298 AA; 32955 MW; CB689
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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273; Conservative
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01-JUN-1998 (TIEMBLIFEL 23, L
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ADP/AIP translocase, Dashit
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Pfam; PF00155; mito_carr; 3.
Pfam; PF00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCARRIER; 3.
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MEDLINE-22035902; PubMed-12006978;

MEDLINE-22035902; PubMed-12006978;

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Methodology Pubmed-12006978;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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EMBL; AF506216; AAM34660.1; ".
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essential for early vertebrate development.";
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Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7955;
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Interpro; IPR002030; Mit_uncoupling.
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(A) CRAWFORD M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.

(A) CRAWFORD M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.

(A) Taxenopus Adenine Nucleotide Translocase mRNA Exhibits Specification During Development.";

(A) Committed (FEB-2000) to the EMBL/GenBank/DDBJ databases.

(C) I. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

(B) C. I. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

(C) I. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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01-CCT-2000 (TrEMBL)
01-MAR-2003 (TrEMBL)
Adenine nucleotide 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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                                                                                                                   MTDAAISFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKHYKGIMDCVVR
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298 AA; 32901 MW; CAEA32C88164AD78
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 23, Last annotation
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Pred. No. 1.3e
20; Mismatches
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Pred. No. 1.6e
L4; Mismatches
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L.3e-120;
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..6e-120;
.es 15;
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Best Loc
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Q9PRH1;
Q9PRH1;
Q1-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, I
01-MAR-2003 (TrEMBLrel. 23, I
ADP/ATP translocase.
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Q8BVI9;
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Solute carrier family 2
                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK078077; BAC37117.1;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Medulla ob
MEDLINE-22354683; PubMed-12466851;
          Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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  Batrachia;
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3 (TrEMBLrel. 23
rier family 25.
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Rodentia;
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Last annotation updat
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 Neobatrachia;
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Pred. No. 6.8e-120;
0; Mismatches 14;
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Sciurognathi;
          Craniata;
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 Ranidae;
           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
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annotation
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RESULT 8
Q9PRI2
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AC Q9PRI2
D01 9PR
D7 01-M
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RA MILURA II, Ohtani H., Makamila M., ICHIKAWA Y., Saitoh K.;

"The origin and differentiation of the heteromorphic sex chromosomes of recommendation of the sequences of the sequenc
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SEQUENCE FROM N.A.

MEDLINE-99083429; PubMed-9866197;

MIUTA I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

"The origin and differentiation of the heteromorphic sex chromosomes

"The origin and differentiation of the heteromorphic sex chromosomes

L. W., X. and Y in the frog Rana rugosa, inferred from the sequences of

a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

1-1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AB008459; BAA36508.1; -.

EMBL; AB008459; BAA36509.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Emphibla; Batrachia; Annra; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PRH2
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88.6%; Pred. No. 1.9e-119;
Live 19; Mismatches 15; Indels 0
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RESULT 9
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AC Q9YIC4
DT 01-W
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                                                                                                                                                                                                                                                           MAINTEDLINE—9008429; PubMed=9866197;

X Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

X Inter Total And differentiation of the heteromorphic sex chromosomes of z., W. X, and Y in the frog Rana rugosa, inferred from the sequences of z., W. X, and Y in the frog Rana rugosa, inferred from the sequences of z., W. X, and Y in the frog Rana rugosa, infection the sequences of z., W. X, and Y in the from the sequences of z., W. X, and Y in the from the sequences of z., W. X, and Y in the from the sequences of z., W. X, and Y in the from the sequences of z., W. X, and Y in the from the sequences of z., W. X, and Y. X, and Y. X. X, and Y. X, and Y. X. 
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InterPro; IPR002067; Mit__carrier.
InterPro; IPR002303; Mit_uncoupling.
Pfam; PF00153; Mitc_carr; 3.
PRINTS; PR00926; MITCCARRIER.
PRINTS; PR00784; MITCCH_CARRIER; 3.
PROSITE; PS00784; MITCCH_CARRIER; 3.
MEMBERANCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPYIC4 PRELIMINARY; PRT; 290 Am.
(DYIC4;
(D1-MAY-1999 (TrEMBLrel. 10, Created)
(1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
(11-MAY-1903 (TrEMBLrel. 23, Last annotation updat
ADP/ATP translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana rugosa (Wrinkled frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
NCBI_TaxID=8410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                           262;
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88.3%; Pred. No. 3.6e-119;
tive 20; Mismatches 15;
                                                                                                                                                          90.98;
                                                                                                                      21;
                                                                                                                  Score 1402; DB 13;
Pred. No. 8.3e-119;
1; Mismatches 15;
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Ranidae; Rana.
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Best Local S
Matches 243
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Q95VX4;
Q95VX4;
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF401758; AAL02100.1; -.
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Pleurostigmophora; Scolopendromorpha;
NCBI_TaxID=62613;
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      Q91336
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      PRELIMINARY;
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81.5%;
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Last sequence update)
Last annotation updat
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Pred. No. 1.5e-109;
6; Mismatches 29;
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      PRT;
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Scolopendridae;
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RESULT 12
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1999) to the MITOCHONDRIAL CARRIER FAMI.
1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI.
R EMBL; U44832; AAA97882.2; -
R InterPro; IPR00193; Mitoch_Carrier.
R InterPro; IPR002067; Mit_Carrier.
R Pfam; PF00153; mito_carr; 3.
R PRIMTS; PR00926; MITOCH_CARRIER.
R PROSITE; PS00215; MITOCH_CARRIER: 3.
Membrane; Transmembrane; Transport.
M Membrane; Transmembrane; Transport.
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Best Local
                                                                                                                                                                   Q8IRAO;
01-MAR-2003
01-MAR-2003
01-MAR-2003
CG16944-PC.
                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cai Q., Greenway S.C., Storey K.B.; "Differential regulation of the mitochondrial in wood frogs under freezing strees."; Biochim. Biophys. Acta 1353:69-78(1997).
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Amphibia; Batrachia; Anura; N
NCBI_TaxID=45438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91336;
01-NOV-1996 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
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  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                       QSGRKGAEIMYSGTIDCWKKIARDEGGRAFFR
                                                                                                                                                                                                                                                                                                                                                                                                              QSGRKGADIMYTGTVDCWRK1FRDEGGKAFFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQGIIIYRAAYEGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKAGAGREFNGLGDCLAKIFKSDGLKGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFVSWMIAQSVTAVAGFGSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPKEQGF ISFWRGNLANVIRYFPTQALNFGFKDKYKKIFLDNVDKRTQFWRYFAGNLASG
                                                                                                                                                                                         3 (TrEMBLrel.
3 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                PRELIMINARY;
  N.A
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10,
23,
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                                                                                                                                                                                         Created)
Last sequ
Last anno
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Neobatrachia;
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Last sequence up
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Pred. No. 8.2e-106;
9; Mismatches 17;
                                                                                                                                                                                         sequence up
                                                                                                                                                                                                                                                                                312
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a; Ranoidea;
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                                                                                                      Insecta;
                                                                                                                                                                                                               update)
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Ranidae; Rana
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gooayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hrandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hrandon R.C., Bayter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aphayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Byraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Byraktaroglu L., Beasley E.M.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,
RA Doublin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegvan C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Hallshin R., Fillson K.A., Mixon K., Nussen D.R., Pacleb J.M., Nelson D.L.,
RA Shie B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Mang Z.K., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.K., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeh R.F., Zhoge S.M., Noghrefi A., Davies S., Shith H.O.,
RA Yel R.F., Saveri J
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Representation of the control o
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Matthews B.B., Bayraktaroglu L., Campbell K., Misra S., Crosby M.A., Matthews B.B., Brochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Clamp M., Drysdale R., Emmert D., Frise E., Je Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; *Annotation of Drosophila melanogaster genome.*; *Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                     Adams M.D., Celniker
Submitted (MAR-2000)
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                    S.E., Gibbs R.A., Rubin G.M., Vent to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                  Venter C.J.;
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RESULT 13

Q9NHW
ID Q9NHW
AC Q9NHW
DT 01-QC
QT 01-QC
DT 01-QC
DT 01-QC
DT 01-QC
CALLIA
QC ELKER
QC HeOPT
QC ELKER
QC HEOPT
QC CALLIA
QC ELKER
QC FERI
RA CHEN
RA [1]
RP SEQUIT
RA CHEN
RI TA CL
RI SUBMI
CC -1- SUBMI
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Best Local
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Best Local :
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Q9NHW5;
Q1-OCT-2000 (
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submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003484; AAN09267.1; -.
SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP/ATP translocase.
Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 IIYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRWMMQSGR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 ATSLCFVYPLDFARTRLAADTGKGG-QREFTGLGNCLTKIFKSDGIVGLYRGFGVSVQGI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184
126 TSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGII 185
                                                                                                                                                                                                                                                                                                        233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | OGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
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                                                                                                           GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                      LGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMIDCFVRIPKEQ 68
                                                                              GFASYWRGNMANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFLGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Transport 300 AA; 33036 MW; 545
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                              80.1%;
79.5%;
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                                                                                                                                                                                                                                                                                                        24;
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Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                              Score 1235.5; DI
Pred. No. 1e-103
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RESULT
044094
ID 04
AC 04
DT 01
DT 01
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044094;
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01-JUN-1998;
01-MAR-2003
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7237;
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
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Last sequence
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Genetica 0:0-0(1997).

-i-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CA
EMEL; AF025799; AAB87884.1; -.

FlyBase; FB900023237; Dsub\sesB.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.

Pfam; PF00153; mito_carr; 3.

PRINTS; PR00926; MITOCH_CARRIER.

PROSITE; PS00215; MITOCH_CARRIER.

PROSITE; PS00215; MITOCH_CARRIER.

MON TEDE
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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ilarity 80.4%;
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Pred. No. 5e-99;
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Best Local Similarity 100.0%; pred. No. 4.5e-16; Best Local Similarity 100.0%; pred. No. 4.5e-16; Matches 298; Conservative 0; Mismatches 0; Indels 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQY	354-49 349, Application US/09434354 No. 6562563 INFORMATION: NT: Murphy, Anne N. ANT: Clevenger, William ANT: Wiley, Sandra Elleen NT: Andreyev, Alexander Y. ANT: Frigeri, Luciano G. NT: Velicelebi, Gonul NT: Davis, Robert E. DF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING DF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, DF INVENTION: MITOCHONDRIAL C	28 244 15.8 308 3 US-09-318-199-2 Sequence 29 244 15.8 308 3 US-09-503-579-2 Sequence 31 232.5 15.1 320 2 US-08-93-750c-12 Sequence 32 232.5 15.1 320 3 US-09-234-613-12 Sequence 34 226.5 14.7 303 1 US-08-518-878B-37 Sequence 35 226.5 14.7 303 2 US-08-294-522B-36 Sequence 36 226.5 14.7 303 2 US-08-618-878B-37 Sequence 37 226.5 14.7 303 2 US-08-618-878B-37 Sequence 37 226.5 14.7 303 2 US-08-470-868A-37 Sequence 38 226.5 14.7 303 2 US-08-470-868A-37 Sequence 39 226.5 14.7 303 2 US-08-946-719A-37 Sequence 40 222 14.7 303 4 US-09-547-983-37 Sequence 41 221 13.7 306 5 PCT-US94-09799-1 Sequence 42 205.5 13.3 307 2 US-08-807-861A-56 Sequence 43 205.5 13.3 307 3 US-08-946-719A-56 Sequence 44 205.5 13.3 307 3 US-08-946-719A-56 Sequence 59 US-09-547-983-56 Sequence 59 US
0; Gaps 0; KGIVDCIVR 60	IONS	ce 2, Appli ce 2, Appli ce 2, Appli ce 12, Appl ce 12, Appl ce 36, Appl ce 37, Appl ce 4, Appl ce 4, Appl ce 4, Appl ce 4, Appl ce 56, Appl

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Patent No. 6013030

Patent No. 6013030

GEMERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Wallace, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TOURBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48, Application US/09434354

Patent No. 6562563

GENERAL INFORMATION:

APPLICANT: Murpby, Anne N.

APPLICANT: Clevenger, William

APPLICANT: Clevenger, William

APPLICANT: Holeyev, Alexander Y.

APPLICANT: Frigeri, Luciano G.

APPLICANT: Velicelebi, Gonul

APPLICANT: Velicelebi, Gonul

APPLICANT: UNENTION: COMPOSITIONS AND METHODS FOR DETERMINING

TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

FILE REFERENCE: 660088.433

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 54

SOPTWARE: FastSEQ for Windows Version 3.0

LENGTH: 298

TYDE: DET
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US-08-961-871-10
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Best Local Similarity 92.6
Matches 274; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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6013858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.2%; Score 1454; DB 4; Length 298; 92.6%; Pred. No. 5.2e-156;
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APPLICATION NUMBER: US 60/030
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: FEIDET, DONNA M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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PRIOR APPLICATION DATA:
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SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-CCT-1997
OF ASSTRUCTATION. BOO
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
264;
                                                                                                                                                                                         61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                          61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                     91.5%; Score 1412; DB 3; Length 29
88.6%; Pred. No. 2.9e-151;
Live 19; Mismatches 15; Indels
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RESULT 4

US-09-434-354-47

(Sequence 47, Application US/09434354)

Fatent No. 6562563

Fatent INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Murphy, Anne N.
APPLICANT: Miley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, ATTLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: UNMEER: US/09/434,354

CURRENT FILING DATE: 1999-11-03

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 47

LENGTH: 297

TYPE: PRT

ORGANISM: Homo sapien

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US-09-996-243-289
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 CURRENT APPLICATION NUMBER: US/09/96,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR PRIOR PRIOR NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1998-02-25
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Best Local Similarity 87.2
Matches 260; Conservative
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                           APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
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Baker, Kevin P.
Botstein, David
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Grimaldi, J. Christopher
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Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                     Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                       Margaret Ann
art, Timothy A.
                                                                                                                                                                                                                                                                                             Daniel
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87.2%;
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R FILING DATE: 1998-05-
R APPLICATION NUMBER: 6
R FILING DATE: 1998-06-
R APPLICATION NUMBER: 6
R FILING DATE: 1998-06-
R FILING DATE: 1998-06-
        FILING DATE: 1998-UG -
APPLICATION NUMBER: 60
TTTMC DATE: 1998-06-1
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
                                                                                APPLICATION NUMBER: 60/
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-04
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FILING DATE: 1998-04-28
                                                                                                                        APPLICATION NUMBER: 60/1
FILING DATE: 1998-06-16
                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 1998-0
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FILING DATE:
                                         APPLICATION NUMBER: 60/
FILING DATE: 1998-06-17
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PR FILING DATE: 1998-06-17
RR APPLICATION NUMBER: 60/08
RFILING DATE: 1998-06-17
RR APPLICATION NUMBER: 60/08
PR FILING DATE: 1998-06-17

60/089599 60/089600

DR APPLICATION NUMBER: 60/089907
DR FILLING DATE: 1996-06-18
DR APPLICATION NUMBER: 60/089908
DR FILLING DATE: 1998-06-18
DR APPLICATION NUMBER: 60/089947
DR APPLICATION NUMBER: 60/089947
DR FILLING DATE: 1998-06-19
DR FILLING DATE: 1998-06-19

APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18

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US-09-188-930-339
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 469
TYPE: PRT
ORGANIZM: Mouse
US-09-188-930-339
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Matches 88
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Best Local
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 QASIEGAPEVTMSSL--FKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFV-LVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 IDLAVYETLKNAWLQHYAVNSADPG----VFVLLACGTMSSTCGQLASYPLALVRTRMQA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 AYFGVYDTAKGM-----LPDPKNTHIVVSWMIAQTVTAVAG-VVSYPFDTVRRRMMM 240
242 LWRGNGINVLKIAPESAIKFMAYEQMKR--LVGSDQET---LRIHERLVAGSLAGAIAQS 296
                                                                                                                                                          10 KDELAGGIAAAISKTAVAPIERVKILLQVQHASKQIAADKQYKGIVDCIVRIPKEQGVLS 69

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188 RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASR----SNNMCIVGGFTQMIREGGAKS 241
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88; Conservative
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                                                                                                                                                                                                                                                                               20.2%;
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; pred. No. 1.7e-26;
62; Mismatches 111; Indels
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FRAICA BLILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR APPLICATION NUMBER: 60/089952
PRIOR APPLICATION NUMBER: 60/090246
PRIOR APPLICATION NUMBER: 60/090246
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090359
PRIOR APPLICATION NUMBER: 60/090359
PRIOR APPLICATION NUMBER: 60/090429
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR APPLICATION NUMBER: 60/090431
PRIOR APPLICATION NUMBER: 60/090431
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR APPLICATION NUMBER: 60/090431
PRIOR APPLICATION NUMBER: 60/090431
PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090447
PRIOR APPLICATION NUMBER: 60/090472
PRIOR APPLICATION NUMBER: 60/09054
PRIOR APPLICATION NUMBER: 60/09054
PRIOR APPLICATION NUMBER: 60/09054
PRIOR PILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR PRICING NUMBER: 1998-06-25
PRIOR PRICING NUMBER: 1998-06-25
PRIOR PRICING NUMBER: 1998-06-25
PRIOR PRICING NUMBER: 1998-06-25

APPLICATION NUMBER: 60/ FILING DATE: 1998-07-01

60/091360

APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-25

60/090696 60/090862

APPLICATION NUMBER: 60/ FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02

60/091544

FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091519

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; ORGANISM: Mouse US-09-312-283C-339
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated fro
TITLE OF INVENTION: and Methods for Their Us
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
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                                                                                                                                                            Patent No. 6534631 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 339
                                                                                                                                                                                     Sequence 118, App
Patent No. 653463
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Best Local :
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                   APPLICANT: ROSen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PC7/US99/15849
EARLIER FILING DATE: 1999-07-14
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      APPLICATION
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                                                                                                                                                                                                                                                                                                     MQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK 461
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                                                                                                                                                                                                                                                                                                                                             MMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFV-LVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                     IDLAVYETL-----KNTWLQRYAVNSADPGVFVLLACGTISSTCGQLASYPLALVRTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAKEGVAAFYKGYIPNMLGIIPYAG
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                                                                                                                                                                                                      Application US/09482273
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    NUMBER:
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Pred. No. 1.7e-26;
2; Mismatches 111
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; LOCATION: (335)
; OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-118
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                                                                                                                                                                                                    US-09-501-558-2
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 118
LENGTH: 335
                                                                                                                    Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application Patent No. 6403784
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CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
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EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
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EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
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ORGANISM: Homo
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                 LENGTH: 291
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nes 87; Conserv
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QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
                                                             KDFLAGGIAAAISKTAVAPIERVKLLLQVQHAS-----KQIAADKQYKGIVDCIVRIPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGVLALYSGIAPALLRQASYGTIKIGIYQSLKRLFVERLEDET-----LLINMICGVVSG
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                                      KPFVYGGLASITAECGTFPIDLTKTRLQIQGQTNDAKFKEI----RYRGMLHALVRIGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNORAIVGHVDLYKGTVDGILKMWKHEGFFALYKGFWPNWLRLGPWNIIFFITYEQLKRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mathur, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Turner, C.
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                                                                                                                                       Score 283.5; DB '
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Pred. No. 6.9e-24;
                                                                                                                      Mismatches
                                                                                                                                                          DB 4;
                                                                                                                      129;
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                                                                                                                      Indels
                                                                                                                                                          Length 291;
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                                                                                                                    31;
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161 124 106 64

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62 124

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Sequence 4, Application US/09160119A
PATCENT NO. 6316219
GENERAL INFORMATION:
APPLICANT: KRIEF, STEDHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: SOUCHET, MICHEL
APPLICANT: BALL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-3985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
CURRENT FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER APPLICATION UNMBER: EP 98401655.0
EARLIER APPLICATION UNMBER: EP 98401655.0
EARLIER APPLICATION UNMBER: EP 98401655.0
EARLIER APPLICATION UNMBER: SEP 98401655.0
RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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; TENGTH: 447
; ORGANISM: HOMO SAPIENS US-09-160-119-4
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                                                                                                                                                                                                                       320 LQVAARAGQTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYEL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAV-AGVVSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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                                                                                                                                                                                                                                                                                                                                                                              262 FLRDIPFSAIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIKTR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ch 18.1%; Score 280; DB 4; Length 447;
1 Similarity 27.1%; Pred. No. 5.1e-23;
80; Conservative 47; Mismatches 148; Indels 20; Gaps
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                                                                                                                                                                                                                                                                                                    MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEL 294
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APPLICANT; KRIEF, STEPHANE
APPLICANT; SORCHET, MICHEL
APPLICANT: SORCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: 6H-30085
CURRENT FILING DATE: 1998-09-24
EARLIER FILING DATE: 1998-09-24
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
TYPE: DET
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                                                                                                                        NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANIZM: HOMO SAPIEN
US-09-142-565-2
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER FILING DATE: 1997-03-16
EARLIER FILING DATE: 1997-03-16
EARLIER APPLICATION NUMBER: 9705614.7
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Best Local S
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                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee James Beeley APPLICANT: Kelly Paine APPLICANT: Robert James
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                     17.2%;
27.1%;
                     Score 265; DB 3; Length 312; Pred. No. 1.5e-21;
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Query Match Best Local S

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US-08-518-878B-56
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                                                                                                          US-08-518-878B-56
                                    Matches
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Best Local 9
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                                                                                                                                                                                             TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: COruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/518,878B FILING DATE: 23-AUG-1995 CLASSIFICATION: 435
                                                                                                                            TOPOLOGY: un
                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56, Application US/08518878B
o. 5702902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 TMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQGENQAVQTARLVQYRGVLGTILTMVRT
12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10036-2711
                                                       Similarity
                                                                                                                                                          amino acid
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                                                                                                                                                                            299 amino acids
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VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
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                                                     16.2%;
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                                  Score 250.5; DB 1;
Pred. No. 6e-20;
2; Mismatches 146;
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 68
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US-08-470-868A-56
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                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
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                  67
                                                                                                                   12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL
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                                                                                                                                                                                                                                                                               amino acid
                SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV
                                               SEWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL
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212) 869-8864
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                                                                                                                                                                      16.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         30,742
                                                                                                                                                        52;
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                                                                                                                                                        Mismatches
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Including Obesity

298

Length Indels

299;

25;

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US-08-518-8788-51
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIDM TYPE: Floppy disk

MEDIDM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/518,878B

FILIMS DATE: 23-AUG-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-036

TELEPHONE: (212) 790-990

TELEPHONE: (212) 790-990
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GENERAL INFORMATION:
APPLICANT: Tartag
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Best Local S
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                 Match 16.2%; Score 250.5; DB 1; Length 309; Local Similarity 24.9%; Pred. No. 6.3e-20; es 74; Conservative 52; Mismatches 146; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
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                                                                                                                                          129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
     191 CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM--- 243
                                                                                              132 AVAOPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 190
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5. 5702902
                                               189 AAYFGYYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS 242
                                                                                                                                                                                                                                                                                                                                     12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
                                                                                                                                                                                            77 SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 131
                                                                                                                                                                                                                                            69 SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
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1155 Avenue of the Americas
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Search completed: August 18, 2003, 16:15:11 Job time : 30 secs

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US-09-815-904A-31
US-09-185-904A-31
US-09-185-904A-31
US-09-734-569-17
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US-10-128-714-338
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Sequence 33, Appl
Sequence 33, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 27, App
Sequence 270, App
Sequence 338, Ap
Sequence 27, Appl
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	-09-997-428-2	US-09-993-667-289	-09-997-653-28	US-09-989-734-289	US-09-993-687-289	US-09-990-436-289	US-09-989-730-289	US-09-991-181-289	US-09-990-444-289	US-09-989-735-289	US-09-989-293A-289	US-09-992-598-289	US-09-989-721-289	US-09-990-456-289	6	-09-99	-09-99		09-98	US-09-989-731-289	US-09-989-727-289	US-09-989-279-289	US-09-989-723-289	US-09-989-722-289	US-09-777-921A-5	US-09-777-921A-2	US-09-777-921A-4	761-364	US-09-925-301-1459
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/811,094; CURRENT FILING DATE: 2001-03-14; NUMBER OF SEQ ID NOS: 37; SOETWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 33; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapien
US-09-811-094-33
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APPLICANT: Davis, Rob
APPLICANT: Clevenger,
APPLICANT: Wiley, San
APPLICANT: Willer, Sc
APPLICANT: Szabo, Tom
APPLICANT: Ghosh, Sov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/09811094 Patent No. US20010044144A1
                                                                                                                                   Matches 298;
                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D4
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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                                                                                     1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                   h 100.0%;
Similarity 100.0%;
98; Conservative 0;
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Pei, Yazhong
                                                                   MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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Pred. No. 6e-157;
Nismatches 0;
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121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ADDETE.

APPLICANT: Davis, Robert E.

APPLICANT: Materson, Christen M.

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Scabo, Tomas R.

APPLICANT: Scabo, Tomas R.

APPLICANT: Moos, Walter H.

APPLICANT: Moos, Walter H.

APPLICANT: Pet, Yazhong

APPLICANT: Moos, Walter H.

APPLICANT: Pet, Yazhong

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 650088 42003

CURRENT APPLICATION NUMBER: US/09/810,644

CURRENT APPLICATION NUMBER: US/09/810,644

CURRENT FILING DATE: 2001-3-14

NUMBER OF SEQ ID NOS: 37

SEQ ID NOS: 37

SEQ ID NOS: 37

LENGTH: 298

TYPE: PRT

GGANISM: Homo sapien
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US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1
                                                                                                   RESULT 3
US-09-185-904A-33
              Sequence 33, Application US/09185904A Patent No. US20020177185A1 GENERAL INFORMATION: APPLICANT: Anderson, Christen M. APPLICANT: Anderson, Christen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
  APPLICANT:
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Davis, Robert E.
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SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
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US-09-811-094-32
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEO ID NOS: 33
            Query Match
Best Local Similarity
                                                                                            TYPE: PRT
ORGANISM: Homo sapien
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            94.2%;
              Score 1454; DB 9
Pred. No. 2e-147;
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Sequence 32, Application US/09811094
Patent No. US20010044144A1
Patent No. US20010044144A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Willer, Robert E.
APPLICANT: Willer, Scott W.
APPLICANT: Woos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
APPLICANT: Pel, Yazhong
APPLICANT: Pel, Yazhong
APPLICANT: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 66088.42014
CURRENT PILING DATE: 2001-03-14
CURRENT FILING DATE: 2001-03-14
UNDBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
SEQ ID NO 32
LENGTH: 298
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APPLICANT: Wiley, Sandra Elleen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Gbosh, Soumitra S.
APPLICANT: Gbosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VQGIIIYRAAYFGVYDTAKGMLPDDKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM 240
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RESULT 5
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US-09-810-644-32
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Scabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088 420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                ocal
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No. US20020012992A1
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                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                               MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
   QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYLPDELKK 296
                                                            GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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Pei, Yazhong
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                                                                                                                                                                                                                                                                                                                          94.2%;
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                                                                                                                                                                                                                                                                                                                          Score 1454; DB 9
Pred. No. 2e-147;
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Sounitra S.
ITILE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
ITILE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
ITILE OF INVENTION: THEREFOR
FILLE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTMARE: FastSEQ for Windows Version
SEQ ID NO 32
LENGTH: 298
TYPE: PDT
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; ORGANISM: Homo
US-09-185-904A-32
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Best Local S
Matches 274
                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                  Patent No. US20010044144A1
                                           APPLICANT: MOOS, Walter H.
APPLICANT: Pe1, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.42004
                                                                                                                                                                                                APPLICANT: Anderson, Christen M. APPLICANT: Davis, Robert E.
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
                                                                                                                        APPLICANT:
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                                                                                                                     Wiley, Sandra Eileen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
                                                                                                                                                                                                                                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                                                                                                  Clevenger, William
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Length 298;

0

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180 180

120 120

60

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APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sounitra S.
APPLICANT: Sabb, Tomas R.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Del TAVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FALING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
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: TYPE: PRT
: ORGANISM: Homo sapien
US-09-811-094-31
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US-09-810-644-31
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SEQ ID NO 31
LENGTH: 297
TYPE: PRT
                                                                                                                                                                                                       Query Match
Best Local S
Matches 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Appl Patent No. US2002
                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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121 GAAGATSLCFVYDLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                         260;
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                                                   1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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                                                                                                                                                                                                                          Similarity
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                                                                                                                               Application US/09810644
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                    89.8%; Score 1385.5; DB 9; Length 297;
87.2%; Pred. No. 4.4e-140;
ative 21; Mismatches 16; Indels 1;
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                                                                                                                                                                                                           16; Indels 1;
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                                                                                                                                                                                                             Gaps
  Sequence 252, Application US/09801368; Batent No. US20020128250Al GENERAL INFORMATION:
APPLICANT: Busby, Robert APPLICANT: Gali, Brian APPLICANT: Hecht, Peter APPLICANT: Holtzman, Doug APPLICANT: Madden, Kevin APPLICANT: Maxon, Mary
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US-09-801-368-252
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GERERAL INCOMMATION:
GERERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Scabo, Tomas R.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: THRAFFOR
TITLE OF INVENTION: THRAFFOR
TITLE OF INVENTION: THRAFFOR
FILE REFERENCE: 660088 420
CURRENT FALING DATE: 1998-11-03
SOFTWARE: FastSEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
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US-09-185-904A-31
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Patent No. US20020177185A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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100 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRWMM 239
                                                                                                                            181 VQGIIIYRAAYFGVYDTAKGMLÞDÞKNTHIVVSWMIAQTVTAVAGVVSYÞFÐTVRRRMM 240
                                                                                                                                                                                                         121 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                        121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260;
                                                                                                                                                                                                                                                                                                     61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 89.8%; Score 1385.5; DB 10; Length 297;
Similarity 87.2%; Pred. No. 4.4e-140;
60; Conservative 21; Mismatches 16; Indels 1; Gaps
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US-09-734-569-170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lerchl,
APPLICANT: Renz, A
APPLICANT: Ehrhard
APPLICANT: Reindl,
APPLICANT: Cirpus,
APPLICANT: Bischof:
APPLICANT: Frank,
APPLICANT: Freund,
APPLICANT: Duwenig
APPLICANT: Schmidt,
APPLICANT: Schmidt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 252
LENGTH: 318
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Patent No. US20020064816A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT:
APPLICANT:
APPLICANT: Reski, Raif
TITLE OF INVENTION: Moss genes from Physcomitrella patens
TITLE OF INVENTION: In the synthesis of carbohydrates
FILE REFERENCE BASF-NAE-1332-99-US
CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/171,101
PRIOR APPLICATION NUMBER: US 60/171,101
PRIOR APPLICATION NUMBER: US 60/171,101
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 LSLLFVYSLDYARTRLAADSKSSKKGGARQFNGLIDVYKKTLKSDGVAGLYRGFLPSVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 TSLCFVYPLDFARTRLAAD--VGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 49.3%; Score 760.5; DB 10; Length Similarity 53.7%; Pred. No. 4.4e-73; 59; Conservative 42; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQA----VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQMIL 312
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                                                                                                                                                                                                                                                                                                                                                                                                            Freund, Annette
Duwenig, Elke
Schmidt, Ralf-Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reindl, Andreas
Cirpus, Petra
Bischoff, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frank, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrhardt, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silva, Jeff
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No. US20020128250Alman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Renz, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Royer, John
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                                                                                                                                                       ; ORGANISM: Aspergillus fumigatus US-10-128-714-3338
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US-10-128-714-3338
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                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PELICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                             SEQ ID NO 3338
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3338, Application US/10128714 Publication No. US20030119013A1
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Best Local S
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LENGTH:
                                                                                                               Query Match
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                                                                             Matches
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8603 SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 GIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 GMMSLWRGNTANVIRVEPTQALNEAEKDYFKSLEGYKKDK-DGYWKWEAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 SSLLFVYSLDYARTRLANDAKSSKKGGGERQFNGLVDVYKKTLATDGIAGLYRGFAISCA
                                                                             154;
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                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIIVYRGLYFGIYDSLKPVVLVGNLEGNFLASFLLGWGITIGAGLASYPIDTVRRRMMMT
                     SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAA---DKQYKGIVDCIVRIPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSLCFVYPLDFARTRLAADV---GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEMTDELMGGVSAAVSKTAAAPIERVKLLIQNQDEMLKSGRLSHPYKGIGECESRTVKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGEA---VKYNGSMDAFKQILAKEGAKSLFKGAGANILRAVAGAGVLSGYDQLQ 373
AFTDSFAVGGVSAAVSKTAAAPIERIKLL--VQNQDEMIRAGRLDRKYNGIIDCFRRTAQ
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                                                                             Conservative
                                                                                           47.88;
51.78;
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                                                                         ; Pred.
47; Mis
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                                                                       Score 737; DB 15;
Pred. No. 1.4e-70;
7; Mismatches 85;
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Pred. No. 8.6e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84;
                                                                                                               Length 308;
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                                                                         Gaps
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APPLICANT: Hu, Weingl
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
ITILE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT EPILICATION UNUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION UNUMBER: US 60/287,066
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION UNUMBER: US 60/287,890
PRIOR APPLICATION UNUMBER: US 60/295,890
PRIOR APPLICATION UNUMBER: US 60/303,899
PRIOR APPLICATION UNUMBER: US 60/316,362
PRIOR APPLICATION UNUMBER: US 60/316,362
PRIOR APPLICATION UNUMBER: US 60/316,362
PRIOR SEQ ID NOS: 8603
SOFTWARE: PRICE 100: 40-28
SOFTWARE: PRIC
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US-10-128-714-8338
Sequence 8338, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Aspergillus fumigatus US-10-128-714-8338
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GATSLLFYYSLDYARTRLANDAKSAKGGGERQFNGLIDVYRKTLASDGIAGLYRGFGPSV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181
241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMCGAFVLVLYDELKKVI 298
                                                                                                     184 LGIVVYRGLYFGMYDSIKPVVLVGSLEGSFLASFLLGWTVTTGAGIASYPLDTIRRRMM 243
                                                                                                                                                                                 182 QGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                             124 GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181
                                                                                                                                                                                                                                                        124 GATSLLFVYSLDYARTRLANDAKSAKGGGERQFNGLIDVYRKTLASDGIAGLYRGFGPSV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 47.8%; Score 737; DB 15; Length 308; al Similarity 51.7%; Pred. No. 1.4e-70; Length 308; 154; Conservative 47; Mismatches 85; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 EQGYLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                              65 AEGVMSLWRGNTANVIRYFPTQALNFAFRDTYKSMFAYKKDR-DGYAKWMMGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AFTDSFAVGGVSAAVSKTAAAPIERIKLL--VQNQDEMIRAGRLDRKYNGIIDCFRRTAQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAA---DKQYKGIVDCIVRIPK 63
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                                   RESULT 15
US-10-259-165-192
; Sequence 192, Applicati
; Publication No. US20030
; GENERAL IMFORMATION;
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Briggs, St
; APPLICANT: Glazebrook
; APPLICANT: Glazebrook
; APPLICANT: Katagiri,
; APPLICANT: Katagiri,
; APPLICANT: Katagiri,
; APPLICANT: Katagiri,
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US-10-141-478A-2
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PRIOR APPLICATION NUMBER: US/10/141/478A
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR APPLICATION NUMBER: 60/289,527
PRIOR PILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 165
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 381
TYPE: PRT
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publication No. US20030148300A1
GENERAL INFORMATION:
APPLICANT: Valentin, Henry
APPLICANT: Valentin, Henry
APPLICANT: Voelker, Toni
APPLICANT: Voelker, Toni
APPLICANT: Lang, Wei
TITLE OF INVENTION: Metabolite Transporters
FILE REFERENCE: 16515-146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 RRMMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 CVGIIVYRGLYFGLYDSVKPVLLTGDLQDSFFASFALGWVI----TNGAGLASYPIDTVR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VQGIIIYRAAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVR 235
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                                   Wang, Xun
Chang, Hur-song
Chang, Hur-song
Briggs, Steven P.
Cooper, Bret
Glazebrook, Jane
Goff, Stephen A.
Katagiri, Fumiyaki
        Kreps, Joel
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APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
ITILE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT PILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 192
LENGTH: 677
TYPE: PRI
COURSEMENT OF SERVING SER
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US-10-259-165-192
Search completed: August 18, 2003, 16:23:10 Job time: 59 secs
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|||||||||||||| :| ::| !| !| !| !| !| !| || || 603 IDTVRRRMMTSGEA---VKYNSSLDAFKQIVAKEGAKSLFKGAGANILRAVAGAGVLAG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 HLPVLVS--LSNRGLYFGMYDSLKPVVLVGNLQD----NFLASFLLGWGITIGAGLASYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 GFSVSVQGIIIYRAAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 GAAGACSLFFVYSLDYARTRLANDAKAAKKGGGRQFNGLVDVYRKTLASDGIAGLYPWIQ 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 EQAIS-FAKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQVKGIVDCIVR 60
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370 EKGLSGFMIDFMMGGVSAAVSKTAAAPIERIKLLIQNQDEMIKSGRLSHPYKGIADCFGR 429
                                                                                                                                                                                                                      291 YDELKKVI 298
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